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From: Sent: To: Subject: Li, Ruixiang

Sunday, November 27, 2005 12:15 PM

STIC-Biotech/ChemLib Sequence search of Application No. 10/600,645

Please do a standard search on:

(i).SEQ ID NO: 2 against both commercial and interference amino acid databases;

(ii). SEQ ID NO: 1 and 2 against both commercial and interference nucleic acid databases.

Thank you very much!

Ruixiang Li **GAU 1646 REM 4D75** Mail Box 4C70 (571) 272-0875

P70 (00.00)

2 aa 532 | na 1813

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Searcher: Searcher Phone: Date Searcher Picked up: Date completed: Searcher Prep Time: Online Time:	Type of Search NA# AA#: S/L: Oligomer: Encode/Transl: Structure #: Text: Inventor: Litigation:	Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM: WWW/Internet: Other (Specify):
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Number of Scarches:	A.A. Sequence	Geninfo
Number of Databases:	Structure Bibliographic	DARC/Questel Other CG7

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STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Ruixiang Li

Art Unit: 1646

Location: rem/4D75/4C70 Serial Number: 10/600645

Monday, December 12, 2005

From: Beverly Shears

Location: Biotech-Chem Library

REM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_New).

Published_Applications_AA_New).



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Wozney,J.M., Celeste,A.J., Thies,R.Scott. and Yamaji,N.
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Patent: Us 6291206-A 1 18-SEP-2001;
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Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Rattus.
                      CACADATGADGTTGACATACCCTTGADCACCAGGGTGGGCACCCAGGCGGTACATGCCCCC
   TAAGAAAATGGTAGTTGCTGTATTGCTGACCTGGGCCCTAGCTGTTAAATTCAACAGTGA
                                                                            CTACAGCTTTGGTTTGATCATTTGGGAGATGGCCCGTCGCTGTATTACAGGAGAATCGT
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                                                                  AGAAGTGCTGGACGAGGACCTGAGTAAAAACCATTTCCAGCCCTACATCATGGCTGACAT
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Antibodies specific for sclerostin and methods for increasing mineralization
Patent: WO 2005014650-A 90 17-FEB-2005;
Celltech R & D, Inc. (US)
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CS027157

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/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"

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llarity 99.6%; Pred. No. 0;
Conservative 0; Mismatches
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CCATGGTACTGGTATGAAATCAGACGTGGACCAGAAGAAGCCGGAAAATGGAGTGACGTT
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                                                                          AGCACCAGAGGACACCTTACCTTAAAATGCTATGCTCAGGACACTGCCCAGATGA
                                                                                        CAACCAATATTTGCAGCCTACACTGCCCCCTGTCGTTATAGGCCCCATTCTTTGATGGCAG
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	750 TGCCAAACAGATTCAGATGGTTCGCAGGTTGGTAAGGCCCGTATGCAGAAGTATGGAT 809 772 TGCCAAACAGATTCAGATGGTTCGCAGGTTGGTAAGGCCCGTATGCAGAAGTATGGAT 831 810 GGGTAAATGCCGTGAAAAAGTGGTTGGTAAAGTATTTTTACCACTGAAGAAGTAGGT 831 812 GGGTAAATGCCGTGAAAAAGTGGCTGTCAAAGTATTTTTACCACTGAAGAAGTAG 809 813 GGGTAAATGCCGTGAAAAAGTGGCTGCCAAAGTATTTTTACCACTGAAGAAGTAG 801 810 CTGGTTTAGAGAAACAGAAATCTACCAGACGGTGTTAATGCGTCATGAAAATAACTTGG 929 811 GGGTTAAAGGAAACAGAAATCTACCAGACGGTGTTAATGCGTCATGAAAATAACTTGG 929 812 CTGGTTTAGAGAAACAGAAATCTACCAGACGGTGTTAATGCGTCATGAAAATAACTGG 921 813 TTTTATAGCTGCAACATAAAGGCACCGGTTCCTGGACTCAGCTGTATTTGATTACTGA 989 814 TTTATAGCTGCAGCATTAAAGGCACCGGTTCCTGGACTCAGCTGTATTTGATTACTGA 989 815 TTTATAGCTGCAGCATTAAAGGCACCGGTTCCTGGACTCAGCTGTATTTGATTACTGA 1011 816 TTACCATGAGAATGGGTCTCTTATGACTTCCTGAAATGTGCCACCAGAGC 1071 817 CCTACTCAAGTTAGCTTCTTGACTTCCTGAAATGTGCCACCAGAGC 1071 818 CCTACTCAAGTTAGCTTATTCTGCTGCCTGTGGTCTGTGCCCCCCACAGAATTTA 1109 819 CTTACCATGAGATTAGCTTATTCTGCTGCTGTGTGTGTGCCCCCCCACAGAAATTTA 1109 810 CTGCTCCAAGTTAGCTTATTCTGCTGCTGTGGTCTGTGCCCCCCCACAGAAATTTA 1131 811 TGGCACGCAAGGCAATGCTCATGACTTGTGGCTGTGTGTG

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/gene="rALK-3"

93. :1681

/gene="rALK-3"

/gene="rALK-3"

/gene="rALK-3"

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kinase domain at nt 788-1663 (AA 153-176), N-linked

91ycosylation site at nt 299-301."

/codon start=1

/product="bone morphogenetic protein type IA receptor"

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Submitted (26-AUG-1994) Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental University, Department of Biochemistry; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)
On Jun 29, 1996 this sequence version replaced gi:599585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 TGGCCCGGACAGGACACGTGCGAATTGGACAATGACTCAGCTATACACTTACATCAGATT
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/strain="Wistar"
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/cell_line="RPC-C2A"
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Best Local Similarity 99.6%;
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Qy 1530 TGAATGTCTTCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCATAATCCAGCATC 1589 Db 1552 TGAATGTCTTCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCATAATCCAGCATC 1611 Qy 1590 CAGACTCACAGCTTTGAGAATCAAGAAGCCTCGCAAAGATGGTTGAATCCCAGGATGT 1611 Db 1612 CAGACTCACAGCTTTGAGAATCAAGAAGCTCGCCAAGAAATCCAGGATGT 1670 AAAGATTTGACAAACAGTTTTGAGAAAGAATTTAGACTGCCAAGAAATTCACCCGAGGAAG 1709 Db 1672 AAAGATTTGACAAACAGTTTTGAGAAAGAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1709 Db 1672 AAAGATTTGACAAGAATTTGAGAAGAATTCAGATTCCCCCAAGAAATTCACCCAAGAAGAATTCACCAAGAAATTCACCAACATAGAATTTAGACTGCTTTCCAAGAAATTCACCAAGAAATTCAAGAATTCACCAAGAAATTCACCATCTTCACCATCTTCACATTTAGAATTCACAAGAAATTCACAACATTACAAGAATACATTCAGAATTCACCAAGAATTCACAACATAAACCTTTCAGAATTCCAAGACTTCACCACTTCACAAATTCACAAAATTCAAGAATACAAAAATTCAAGAAATCCAAAATCCAAAATCCAAAATCCAAAATCAAAAAAA	PERBULT 6 DETAILION Sequence 119 from Patent W0205001188. Inhear PAT 25-JAN-2005 DETAILION Sequence 119 from Patent W0205001188. Inhear PAT 25-JAN-2005 DETAILION Sequence 119 from Patent W0205001188. Inhear PAT 25-JAN-2005 DETAILION C0986810. G1:58194649 SOURCE REPRENCE PATENCY PA	OY 330 TCAGGAGAAACCACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG 389

375 AGCACCAGAGGACACCTTACTTAAAATGCTATTGCTCAGGACACTGCCCAGATGA 434 270 CGCTATTAATAACACATGCATAACTAATGGCCCATTTGCCATTATAGAAGAAGATGA 329 435 CGCTATTAATAACACATGCATAACTAATGGCCATTGCTTTTGCCATTATAGAAGAAGATGA 494 330 CGCGAACAACCACGTTAACTTCTGGGTCTATTGCCATTATAGAAGAAGATGA 494 349 CGCGAACAAACCACGTTAACTTCTGGGTCTATGAAGGCTCTGATTTTCAATG 389 495 TCAGGGAAAACCACGTTAACTTCTGGGTGTATGAAGGTTTGTCGATTTTCAATG 554 390 CAAGGATTCACCAAAAGCCCAGCTACGCAGACAATAGAAGGTTTGTCGATTTTTTTT	630 CCGTGACTTGGAACAGGATGAAGCATTTATTCCAGTAGGAGAATCACTGAAAGACCTGAT 6 [975 GGGTAAATGGCCGTGGTGAAAAGTGCTGTCAAAGTATTTTTTTACCCTGAAGAAGCTAGGAAATAAAGGAAAATAAAGGCAGGGTGTTAATGGCTCATGAAAATATACTTAGGGAAAATAAAGGCACCGGTTAATAAGGCTCAGGAAATAAAGGCACCGGTTCCTCGGACTCAGCTGAAATATACTTAGATAACTAGAGAAAGGCACCGGTTCCTCGACTCAGCTGAATTTGATTACTTCAGGAATGGCTCCTCGAAATGCTCCTCGAAATGATAAAGGCACCCGGTTCCTCGAAATGACTACCTAGAATAAGGCACCCGGTTCCTGAAATGATTAGATTAGATTACTTCAGGAATGGGTCTCTCTAAGACTCCTGAAAATGTGCCCCCCTGGAAATGACTACCTAGAATGACTTCCTGAAATGTGCCCCCCTGGAAATGACTCCTAAAAGGCACCCTGAAATGTGCCTCCTAAAAGGCACCCTGGAAATGTGCCACCCTGGAAACCAGAGC 1214	1050 CCTACTCAAGTTAGCTTATTCTGCTGGTGGTCTGTGCCACCTCCACAGAAATTTA 1215 CCTACTCAAGTTAGCTTATTCTGCTGGTCTGTGCCACCTCCACCACAGAAATTTA 1110 TGGCACGCAAGGCAAGCCTGCATTGGTCATCGAGACCTCGAAGCAAAACTTTA 1110 TGGCACGCAAGGCAAGCCTGCAATTGCTCATCGAGACCTGAAGAGCAAAAACATCCTTAT 1170 TAAGAAAAATGGTAGTTGCTGAATTGCTGACCTGAAGAGCAAAAAATCAACTGTAT 1131 TAAGAAAAATGGTAGTTGCTGAATTGCTGACCTGGGCCTAGGTTAAATTCAACAGTGA 1335 TAAGAAAAATGGTAGTTGCTGTATTGCTGACCTGGGCCTAGCTGTAAATTCAACAGTGA 1230 CACAAATGATGCTGTATTGCTGACCTGGGGCCTAGCTGTAAATTCAACAGTGA 1230 CACAAATGATAGCTGCTGTATTGCTGACCTGGGGCCTAGCTGTTAAATTCAACAGTGA 1230 CACAAATGATAGCTGCTGTATTGCTGACCTGGGGCCTAGCTGTTAAATTCAACAGTGG 1231 CACAAAATGATAGCTGACTTGAACACTGGGGCCTAGCTGTTAAATTCAACAGTGG 1231 CACAAAATGATAGCTGATATTGCTGACCTGGGGCCTAGCTTGATAATTCAACAGTGG	1395 CACAMATIGACATIGACCTTGAACACCACCAGGGGGGGGGGGGGG
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GGAGGAATATCAATTACCATATTACAACATGGTGCCTAGTGACCC	3-MAR-2	NCE ORS E NAL NAL	ORIGIN Query Match Query Match Best Local Similarity 99.6%; Score 1750.4; DB 6; Length 3167; Best Local Similarity 99.6%; Pred. No. 0; Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2; Oy 30 TGCGGCCGCAGGACACGTGCGAATTGGACAATGACTCAGCTATACATCAGATT 89	315 CCATGGTACTGGTATGAAATCAGACGTGGACGTGAAGCCGGAAAATGGGTGACGTT 374 210 AGCACCAGAGGACCCTTACCTTTCTTAAAATGCTGATGACCTGCCCAGATGA 269

315 CCATGGTACTGGTATGAAATCAGACGAGAAGAGCCGGAAAATGGAGTGACGTT 374 210 AGCACCAGAGGACACCTTACCTTTCTAAAATGCTATTGCTCAGGACACTGCCCAGATGA 249 375 AGCACCAGAGGACACCTTACCTTTCTTAAAATGCTATTGCTCAGGACACTGCCCAGATGA 339 376 AGCACCAGAGGACACCTTACTATTGCTATTGCAGCACTGCCCAGATGA 340 377 CGCTATTAATAAAACACTACTAATGGCCATTGCTTTGCCATTATAGAAGAAGATGA 340 378 CGCTATTAATAACACCATTACTACTATAGAACTATTACAAGAAGATGA 340 379 CGCTATTAATAACACTACCATAACTAATGAACTATTGCCATTATTGAAGAAGATGA 340 380 CAGGGAAAACCACGTTAACTTCTGGGGCCATTATTGAAGAAGATGA 340 380 CAAGGATTCACCAAAAGCCCAGCTACGAGACATATAAAAGAAGAAGATGA 340 380 CAAGGATTCACCAAAAGCCCAGCTACGAGACAATAGAATGTTGTCGGACCAATTTTCAATG 350 380 CAAGGATTCACCAAAAGCCCAGCTACGCAGGACAATAGAATGTTGTCGGACCAATTTTTCAATG 360 380 CAAGGATTCACCAAAAGCCCAGCTACGCAGGACAATAGAATGTTGTCGGACCAATTTTTTAATGAGAGAGA	CCGTGACTTCTGTTACAAACATTACTGTAAGAGTATCTCAAGCAAG	915 GGGTAAATGGCGTGGAAAAAGTGGCTGTCAAAGTATTTTTACCACTGAAGAAGTGG 819 975 GGGTAAATGGCGTGGAAAAAGTGGCTGCAAAGTATTTTTACCACTGAAGAAGCTAG 1034 870 CTGGTTTAGAGAACAGAATCTACCAGACGTGTTAATGCGTCATGAAAATATACTTGG 929 1035 CTGGTTTAGAGAAACAGAATCTACCAGACGGTGTTAATGCGTCATGAAAATATACTTGG 929 1036 TTTTATAGCTGCAGAAATCTACCAGACGGTGTTAATGCGTCATGAAAATATACTTGG 1094 930 TTTTATAGCTGCAGACATTAAAGGCACCGGTTCCTGGAACTCAGGACTTTGATTACTGA 989 1154 TTTATAGCTGCAGACATTAAAGGCACCGGTTCCTGGAACTCAGGACTGTATTTGATTACTGA 1154 1095 TTTTATAGCTGCAGACTTTAAAGGCACCGGTTCCTGGACTCCTGGACTCTGTATTTACTGA 1154 1155 TTACCATGAGAATGGGTCTCTCTATGACTTCCTGAAATGTGCCACCCTGGACACCAGAGC 1214 1155 TTACCATGAGAATGGGTCTCTCTATGACTTCCTGAAATGTGCCCCTGGACACCAGAGC 1214	1050 CTACTCAAGTTAGCTTATTCTGCTGGTCTGTGCCACCTCCACACAAATTTA 1109
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1350 CTACAGCTTTGGTTTGATCATTTGGGAGATGGCCCGTCGCTGTAN	OY 1770 TCACAGGCTGCTAACGTTAAACCTTTCAGGACTCTGCAGAATGC 1813	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. REFERENCE AUTHORS Winkler, D.G., Shi,J. and Latham,J. TITLE Antibodies specific for sclerostin and methods for increasing bone mineralization JOURNAL Patent: WO 2005014650-A 89 17-FEB-2005; Celtech R E D, Inc. (US) FEATURES Location/Qualifiers Location/Qualifiers //Organism="Rattus norvegicus" //mol_type="unassigned DNA" //db_xref="taxon:10116"	Query Match 96.5%; Score 1750.4; DB 6; Length 3167; Best Local Similarity 99.6%; Pred; No. 0; Additional and a conservative 0; Mismatches 6; Indels 2; Gaps 2; Qy 30 TGCGCCGGACAGGACACGTGCGAATTGGACAATGACTAACACTACATTACATCAGATT 89 10 11 <t< td=""></t<>

/ db_xref="GI:834008" / trainslation="MTOLYTYIRLLGACLFIISHVQGONLDSMLHGTGMKSDVDOKKP RNGVTLAPEDTUPFLKCYCSGHCPDDAINTCTTNGHCFAIIEEDDQGETTLTSGCMK YEGSBPCFCAEPERAQLERTIECCTRTNCHCOYLOPTLPPVUGEPEDGSVMLAAVLISM AVCIVAMIVFSSCFCAFHYCKSISSRGRYNRDLEODEAFIPVOGFTDETDGSOSSGS GSGLPLLVQRTTAKQIQMVRQVGKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETE IYQTTAKRHENTIGFIFAADIKTGSWRQLYLITDFRANGSLYPPERCACATORDLIDGSOSSGS ASAACGLCHUHTEIYOTGCRAAIAHDLKSKVAILIKKNGSCCIADLGLAVKFNSDTN EVDIPLNTRVGTRRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIWEMARRCITGGIV BEYQLPYYNMVPSDPSYEDMREVVCVKRLRPIVSNRWNSDECLRAVLKLMSECWAHNP ASRLTALLRIKKTLAKMVESQDVKI"	Query Match 96.5%; Score 1750.4; DB 9; Length 3167; Best Local Similarity 99.6%; Pred. No. 0; 0.	DB 199 IGGCCCGGARAGGARACGICCGARITGGACAGIGACICAGGIAIACACTIRAGICAGATI 254 Qy 90 ACTGGGAGCCTGTCTTCATCATTTCTCATGTTCAAGGGCAGAATCTAGATAGCT 149 Db 255 ACTGGGAGCTGTTCATCATTTCTCATGTTCAAGGGCAGAATCTAGATAGCT 314 Qy 150 CCATGGAAGATCAAACAGGGGGAACCGGAAAATGGATCGAGGTGAACTAGATTCAGAGGGAGG	315 CCATGGTATGAAATCAGAGGGACCAGAAGAGGGAAATGGAGAGGGGTGACGTT 374	OY 270 CGCTATTAATAACACATGCATAACTAATGGCCATTGCCTTTGCCATTATAGAAGAAGATGA 329	0y 310 TCAGGAGAAACCAGGTAACTTCTGGGTGTATGAAGGCTCTGATTTTCAATG 319 1
Oy 1290 AGAAGTGCTGGACGAGGCTGAGTAAAAACCATTTCCAGCCCTACATGGCTGACAT 1349		1590 1755 1650	Db 1815 AAAGATTTGACAAACAGTTTTGAGAAAGATTTAGACTGCAAGAAATTCACCCGAGGAAG 1874 Qy 1710 GGTGGAGTTAGCATGGACTAGGATGTGGCTTGGTTTCCAGACTCTCTCT	Oy 1770 TCACAGGCTGCTAACACTTTCAGGACTCTGCAGAATGC 1813 	RESULT 10 S75359 LOCUS DETINITION S75359 S75359 ACCESSION S75359 LOCUS DETINITION S75359.1 GI:834007 KEYNORDS SARIUS 8P. ACTESSION S75359.1 GI:834007 KEYNORDS SOURCE RATUS 8P. SARIUS 8P. SARIUS 8P. SARIUS 8P. ACTESSION S75359.1 GI:834007 KEYNORDS SOURCE RATUS 8P. ACTESSION RATUS 8P. SARIUS 8P. ACTESSION S75359.1 GI:834007 REFERENCE RATUS 8P. ACTESSION AMMALIA ENATIONALIA (ALTA ENATIONALIA (AL

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Direct Submission
Submitted (16-SEP-1993) Hiroshi Takahashi, Tokyo Metropolitan
Institute of Gerontology, Department of Pathology; 35-2 Sakaecho,,
Itabashi-ku, Tokyo 173, Japan (Tel:03-3964-3241(ex.3034),
Pax:03-3579-4776)
                                                                    merphogenetic protein 4 receptor
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                           /tissue type="brain"
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/dev_stage="embryo"
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/clone="rB4r1"
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Ikeda,T. and Takahashi,H.
Expression pattern of bone embryo and adult rat
Unpublished
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04-FEB-1999

ROD 04-FEB-19 complete cds.

mRNA linear protein 4 receptor,

RAINBARI 1599 bp mRN Rat mRNA for bone merphogenetic protein 1767.1 GI:684975 bone merphogenetic protein 4 receptor. Rattus norvegicus (Norway rat)

RESULT 11
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ASRLTALRIKKTLAKMVESQDVKI
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Mus musculus
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Best Local Similarity 94.2%;
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1 (basea 1 to 2292)
Suzuki,A., Thies,R.S., Yamaji,N., Song,J.J., Wozney,J.M., Murakani,K. and Ueno,N.
A truncated bone morphogenetic protein receptor affects dorsal-ventral patterning in the early Xenopus embryo Direct Submission
Submitted (13-MAY-1993) Naoto Ueno, Hokkaido University, Faculty of Pharmaceutical Sciences, Sapporo, Hokkaido 060, Japan (Tel:81-11-716-8513, Fax:81-11-716-8513)
Location/Qualifiers 1501 TCAGAATGCTGGGCCCATAATCCAGCATCAGAATCAGAATCAAGAAGG TCAGAATGCTGGGCCCATAATCCAGCATCCAGACTCACAGCTTTGAGAATCAAGAAGACG 39 CAGGACACGTGCGAATTGGACAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC /organism="Mus musculus"
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/clone library of K. Nakayama and M. Hosaka" ROD 6 Length 2292; 94; Indels мовычекс 2292 bp mRNA linear Mus musculus mRNA for BMP receptor, complete cds. D16250 CTCGCAAAGATGGTTGAATCCCAGGATGTAAAGATTTGA 1659 DB 9; Score 1584.6; Pred. No. 0; 0; Mismatches

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Series: IRAK Plate: 53 Row: g Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
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                                                                                                                                                                                                                                                                                                           Contact: MGC help desk.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HSC
Contact: ang@bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                                                                                            Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A. Gencration and initial malysis of more than 15,000 full-length human and mouse cDNA sequences
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                                                                           Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/lab_host="DH10B"
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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/db_xref="GeneuD:12166"
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0; Mismatches
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Best Local Similarity 94.2
Matches 1680; Conservative
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TITLE
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ive 0; Mismatches
    'mol_type="unassigned DNA"
'db_xref="taxon:10090"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurograthi; Muroidea; Muridae; Mus.

Vermashia; Muroidea; Muridae; Murinae; Mus.
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LUDWIG INST CANCER RES (GB)
Other publication CA 2143441 940526
Other publication AU 5432094 940608
Other publication NZ 257631 960506
Other publication OF 8505049T 960604.
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90 A9	1215 GTTAGCTTATTCTGCTGCTGTGTGTGTGTGTGTGTGTGTG	Query Match Best Local Similarity 94.1%; Pred. No. 0; Matches 1678; Conservative 0; Mismatches 99 Oy 39 CAGGACACGGGAATTGGACAATGACTCAGCTATAC	NB 6; Length 2070; 96; Indels 9; Gaps 3; CACTTACATCAGATTACTGGGAGC 98
& a	1179 TGGTAGTTGCTGTATTGCTGACCTGGCCTAGCTGATAAATTCAACAGTGACACAAATGA 1238 	Db 195 CAGGACGCGTGGCAATCACAATGACTCCAGCTATACACTTACATCAGATTACTGGGAGC Qy 99 CTGTCTGGTTCATCATCTTCAAGGGCAGAATCTAGATAGTAGTATGCTCCATGGTAC	
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b o	1359 TGGTTTGATCATTGGGGGATGGCCCGTCGCTGTATTACAGGGGAATCGTGGAGGAATA 1418 	Db 375 GGATACCTTGCCTTTCTTAAAGTGCTATTGCTCAGGACACTGCCCAGATGATGCTATTAA Qy 279 TAACACATGCATAATGGCCATTGCTTTGCCATTATAGAAGAAGATGATGGGGGGA	
e ý	1419 TCAATTACCATATTACAACATGGTGCCTAGTGACCCATCTTATGAAGACATGCGTGAGGT 1478 	Db 435 TAACACATGCATAACTAATGGCCATTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAN Qy 339 AACCACGTTAACTTTCTGGGTGTATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTC	
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} &	1 GTGGAGTTAGCATGGACTAGGATGTCGGCTTGGTTTCCAGACTCTCTCT	OY 5/2 CITCLGIIACAMACATIACIGIAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GAGGCTGCTTACAACCGTGACTT 838
g &	1875 GIGGGATTAGCATGGAATAGGATGTTGGTTTTCCAGACTCCTTCCT	Qy 639 GGAACAGGATGAAGCATTTATTCCAGTAGGAGAATCACTGAAAGACCTGATTGACCAGTC Db 795 GGAACAGGATGAAGCATTTATTCCAGTAGGAGAATCATTGAAAGACCTGATTGACCAGTC	TGAAAGACCTGATTGACCAGTC 698 TGAAAGACCTGATTGACCAGTC 854
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Adx97425 Human bon
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Add53821 DNA used
Add89877 Antagonis
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/product= "Bone morphogenic protein receptor."
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 P-PSDB; AAR70237
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28-SEP-1995
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 Aa209847 Human mAL
Ady51875 Murine AL
Aaq66640 Mouse Act
Aa290184 BRK-1 DNA
Aa127228 Bone morp
Aa128021 Mouse BMP
Aav71972 Mouse BMP
Aav71973 Mouse BMP
Aav71973 Human ALK
Aac06031 Human ALK
Aas87057 DNA eccod
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                                                         9, 2005, 05:59:38 ; Search time 767 Seconds (without alignments) 15753.700 Million cell updates/sec
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1 CTAGTGGATCCCCCGGGCTG......TTCAGGACTCTGCAGAATGC 1813
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         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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kinase receptors may be used in compositions to inhibit the effects of BMP's such as BMP 2 and BMP-4. The truncated receptors pref. comprise the ligand binding domain, but not the serine/threonine kinase and transmembrane domains. The truncated proteins are soluble and will be excreted into supernatant by recombinant mammalian cells expressing them. Such cells can be delivered in a medium or matrix which partially impedes their mobility, thereby localising the cells to a site of bone or cartilage injury. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention can be used for treating osteopenia, osteoporosis, fractures and other disorders related to low bone mineral content and density. As such, these compositions improve bone mineralization and can be described as TGF-beta antagonists and/ or BMP-antagonists. This polynucleotide is a bone morphogenetic protein receptor type I DNA sequence given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel antibody or antigen-binding fragment that binds specifically to a sclerostin (SOST) polypeptide and impairs formation of a sclerostin homodimer. Specifically, it refers to an antibody that competitively inhibits binding of the sclerostin polypeptide to a bone morphogenic protein (BMP) Type I receptor binding site. The present invention describes a hybridoma cell capable of producing the antibody and a host cell for antibody expression. Furthermore, it provides a nucleic acid molecule encoding a transforming growth feator beta (FQF-beta) binding protein known as SOST (and also BEER) and methods for detection thereof Accordingly, such antibodies and osteopathic compositions of the
                                                              receptor; bone morphogenetic protein; bone injury; antibody production; TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias; osteoporosis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody or antigen-binding fragment that binds specifically to sclerostin polypeptide and which inhibits binding of sclerostin polypeptide to a bone morphogenic protein, useful for increasing bone
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                               Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 121.
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                                                                                                                                                                                                                            /product= "BMP receptor type 1 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 121; 205pp; English
                                                                                                                                                                         Location/Qualifiers
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Winkler DG;
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/product= "Rat bone morphogenic protein type I receptor"
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                                                                                                                                                                                                                                                                                                                                                                  antibody; sclerostin; SOST; bone morphogenic protein receptor; Transforming Growth Factor; osteopathic; gene therapy; bone repair; osteopenia; osteoporosis; bone injury; gene; ds.
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The invention relates to a novel isolated antibody, or its antigenbinding fragment, which binds specifically to a sclerostin (SOST)

CC binding fragment, which binds specifically to a sclerostin (SOST)

CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190

or 213 amino acids, fully defined in the specification (ADX97341,

ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408) The antibody

CC competitively inhibite binding of the SOST polypeptide to a bone

morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II

Receptor binding site, where the BMP Type I Receptor binding site is

C capable of binding to a BMP Type I Receptor binding site is

C capable of binding to a BMP Type I Receptor binding site is

C capable of standing to a BMP Type I Receptor binding site is

C capable of standing to a BMP Type I Receptor polypeptide. The invention

C turther comprising the new antibody, or its antigen-binding fragment, and a

C physiological carrier; an immunogen comprising a peptide comprising 6, 7,

B, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of

the SOST polypeptide, methods for producing an antibody that specifically

CC that impairs binding Growth Factor (TGF)-beta signaling pathway,

that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,

CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST

c antibody and compositions have osteopathic activity. The SOST nucleic

c and increasing bone mineralization, which may treat or prevent diseases

C for increasing bone mineralization, which may treat or prevent diseases

C conditions associated with low bone mineral density, such as

C represents a rat bone morphogenic protein type I receptor encoding DNA of

the invention.
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New isolated antibody specific for a sclerostin polypeptide, useful for increasing bone mineralization or for treating or preventing conditions associated with low bone mineral density, e.g. osteoporosis or
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This invention relates to a novel antibody or antigen-binding fragment that binds specifically to a sclerostin (503T) polypeptide and impairs formation of a sclerostin homodimer. Specifically, it refers to an antibody that competitively inhibits binding of the sclerostin polypeptide to a bone morphogenic protein (BMP) Type I receptor binding site or a BMP Type II receptor binding site or a BMP Type II receptor binding site. The present invention describes a hybridoma cell capable of producing the antibody and a host cell for antibody expression. Furthermore, it provides a nucleic acid molecule encoding a transforming growth factor-beta (TGF-beta) binding protein known as SOST (and also BERN) and methods for detection thereof. Accordingly, such antibodies and osteopathic compositions of the invention can be used for treating osteopeneia, osteoporosis, fractures and other disorders related to low bone mineral content and density. We such, these compositions improve bone mineralization and can be described
                                                                                                                                                                                                                                                                                                                                                                   receptor; bone morphogenetic protein; bone injury; antibody production; TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias; osteoporosis; gene; ds.
      CAGACTCACAGCTTTGAGAATCAAGAGACGCTCGCAAAGATGGTTGAATCCCAGGATGT
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                                              GGTGGAGTTAGCATGGACTAGGATGTCGGCTTGGTTTCCAGACTCTCTCCTCCTACCATCT
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                                                                                                                                                                                                                                                                                                                                        Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seg 120
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as TGF-beta antagonists and/ or BMP-antagonists. This polynucleotide bone morphogenetic protein receptor type 1 DNA sequence given in an exemplification of the invention.
                                                                    Gaps
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                                                                   2;
                                   T; 0 U; 0 Other;
                                                                   Indels
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                                                   DB
                                                 Score 1750.4;
Pred. No. 0;
0; Mismatches
                                   BP; 908 A; 647 C; 688 G; 924
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Matches 1776; Conservative
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1514 1709 1634 1814 receptor; bone morphogenetic protein; bone injury; antibody production; TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias; osteoporosis; gene; ds. TGGCACGCAAGGCAAGCCTGCAATTGCTCATCGAGACCTGAAGAGCAAAAACATCCTTAT CACAAATGAAGTTGACATACCCTTGAACACCCAGGGTGGGCCACCAGGCGGTACATGGCTCC AGAAGTGCTGGACGAGGCCTGAGTAAAAACCATTTCCAGCCCTACATCATGGCTGACAT CTACAGCTTTGGTTTGGAGATGGCCGTCGTGTATTACAGGAGGATCGT CTACAGCTTTGGTTTGATCATTTGGGAGATGGCCCGTCGTCTATTACAGGAGAATCGT 1695 TGAATGTCTTCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCATAATCCAGCATC GGTGGAGTTAGCATGGACTAGGATGTCGCCTTGGTTTCCAGACTCTCTCCTCTACCATCT CACAAATGAAGTTGACATACCCTTGAACACCAGGGTGGGCACCAGGCGGTACATGGCTCC TGAATGTCTTCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCATAATCCAGCATC **AAAGATTTGACAAACAGTTTTGAGAAAGAATTTAGACTGCAAGAAATTCACCCGAGGAAG** GGTGGAGTTAGCATGGACTAGGATGTCGGCTTGGTTTCCAGACTCTCCTCCTCTA-CATCT TAAGAAAAATGGTAGTTGCTGTATTGCTGACCTGGGCCTAGCTGTTAAATTCAACAGTGA CAGACTCACAGCTTTGAGAATCAAGAAGACGCTCGCAAAGATGGTTGAATCCCAGGATGT Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seg 119 TCACAGGCTGCTAACAGTAAACCTTTCAGGACTCTGCAGAATGC 1813 BP DNA; 3167 (first entry) standard; 07-APR-2005 1215 1110 1275 1335 1230 1395 1455 1350 1515 1575 1635 1650 1815 1710 1770 1155 1050 1170 1290 1410 1470 1530 1590 1755 1875 1934 990 ADW28815 g ò q ò g S B ò g 8 8 8 음 장 셤 ò a ራ 성 ò g g a g 8 ò ठे ò

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> CGTCCGATGGCTGGCTGTGTCTCTATGGCTGTCTGTATTGTCGCCATGATCGTCTT CTCCAGCTGCTTCTGTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA CTCCAGCTGCTTCTGTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA

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TGCCAAACAGATTCAGATGGTTCGGCAGGTTGGTAAGGGCCCGGTATGGAGTATGGAT

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Pred. No. 0;
0; Mismatches 6; Indels 2;
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                                "BMP receptor type 1 protein"
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                                                                                                                                                                                                                                Disclosure; SEQ ID NO 119; 205pp; English
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                                                                                                   16-JUN-2003; 2003US-00463190
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Winkler DG;
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P-PSDB; ADW28801.
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that binds specifically to a sclerosin. GOST) polypeptide and impairs formation of a sclerostin homodimer. Specifically, it refers to an antibody that competitively inhibits binding of the sclerostin competitively inhibits binding of the sclerostin or polypeptide to a bone morphogenic protein (BMP) Type I receptor binding site or a BMP Type II receptor binding site. The present invention describes a hybridoma cell capable of producing the antibody and a host cell for antibody expression. Furthermore, it provides a nucleic acid molecule encoding a transforming growth factor-beta (TGF-beta) binding protein known as SOST (and also BERN) and methods for detection thereof. Accordingly, such antibodies and osteopathic compositions of the cinvention can be used for treating osteopenia, osteoprosels, fractures and other disorders related to low bone mineral content and density. As such, these compositions improve bone mineralization and can be described to low the state of the low of low of the low of the low of low of the low of lo invention relates to a novel antibody or antigen-binding fragment New antibody or antigen-binding fragment that binds specifically to sclerostin polypeptide and which inhibits binding of sclerostin polypeptide to a bone morphogenic protein, useful for increasing bone mineral content or density. bone morphogenetic protein receptor type 1 DNA sequence given in an exemplification of the invention. BW;

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GGGTAAATGGCGTGGTGAAAAAGTGGCTGTCAAAGTATTTTTTACCACTGAAGAAGCTAG 1034 CTGGTTTAGAGAAACAGAAATCTACCAGACGGTGTTAATGCGTCATGAAAATATACTTGG 1335 TAAGAAAAATGGTAGTTGCTGTATTGCTGACCTGGGCCTAGGCTGTTAAATTCAACACAGTGA 1455 AGAAGTGCTGGACGAGAGCCTGAGTAAAAACCATTTCCAGCCCTACATCATGGCTGACAT TITIATAGCTGCAGACATTAAAAGGCACCGGTTCCTGGACTCAGCTGTATTTGATTACTGA TTACCATGAGAATGGGTCTCTCTATGACTTCCTGAAATGTGCCACCCTGGACACCAGGGC TTACCATGAGAATGGGTCTCTCTATGACTTCCTGAAATGTGCCACCCTGGACACCCGGGGC CCTACTCAAGTTAGCTTATTCTGCTGCCTGTGGTCTGTGCCACCTCCACACAAATTTA. CACAAATGAAGTTGACATACCCTTGAACACCAGGGTGGGCACCAGGCGGTACATGGCTCC cracaccriricerrigarcarricegagareccccricerarracageagaareer TGGCACGCAAGGCAAGCCTGCAATTGCTCATCGAGACCTGAAGAGCAAAAACATCCTTAT TAAGAAAAATGGTAGTTGCTGTATTGCTGACCTGGGCCCTAGCTGTTAAATTCAACAGTGA CACAAATGAAGTTGACATACCCTTGAACACCAGGGTGGGCACCAGGCGGTACATGGCTCC <u> AGAAGTGCTGGACGAGAGCCTGAGTAAAAACCATTTCCAGCCCTACATCATGGCTGACAT</u> 1035 066 1215 1110 1275 1170 1230 1515 975 870 1095 1155 1050 1395 1350 930 1290 엄 ð ò 유 ò 원 셤 ò g g ò ò ò 셤 g ò 셤 ઠે 254 149 314 209 374 269 434 494 83 2; Gaps

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                                                                                                                                                                                               AAAGATTTGACAAACAGTTTTGAGAAAGAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated antibody specific for a sclerostin polypeptide, useful for increasing bone mineralization or for treating or preventing conditions associated with low bone mineral density, e.g. osteoporosis or
GGAGGAATATCAATTACCATATTACAACATGGTGCCTAGTGACCCATCTTATGAAGACAT
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                                                                              TGAATGTCTTCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCCATAATCCAGCATC
                                       GGGTGAGGTGGTGTGTGAAACGCTTGCGGCCAATCGTCTCTAACCGCTGGAACAGTGA
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                               GCGTGAGGTCGTGTGTGTAAACGCTTGCGGCCAATCGTCTCTAACCGCTGGAACAGTGA
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                                                                                                                                                                                                                                                                                                                                                                       antibody; sclerostin; SOST; bone morphogenic protein receptor; Transforming Growth Factor; osteopathic; gene therapy; bone repair; osteopenia; osteoporosis; bone injury; gene; ds.
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binding fragment, which binds specifically to a sclerostin (SOST)
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polypeptide. The SOST polypeptide comprises any of 6 sequences having 190 or 213 amino acids, fully defined in the specification (ADX97341, CC ADX97360, ADX97360, ADX97400, ADX97408). The antibody competitively inhibits binding of the SOST polypeptide to a bone competitively inhibits binding of the SOST polypeptide to a bone competitively inhibits binding of the SOST polypeptide of a bone steep to binding site, where the BWP Type I Receptor binding site is capable of binding to a BMP Type I Receptor bolypeptide. The invention cutrier comprising the new antibody, a composition of further comprising the new antibody, a nost comprising the new antibody, or its antigen-binding fragment, and a composition comprising the new antibody, or its antigen-binding fragment, and a physiological carrier; an immunogen comprising a peptide comprising 6, 7, 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of the SOST polypeptide; and methods for identifying an antibody that specifically compositions are the SOST polypeptide; and methods for identifying an antibody that impairs binding of a BMP to the SOST polypeptide, that impairs SOST compositions have osteopathic activity. The SOST nucleic acids may be used in gene therapy. The composition and methods are useful correctsing bone mineralization, which may treat or prevent diseases or conditions associated with low bone mineral density, such as correcting an art bone morphogenic protein type I receptor encoding DNA of the composition and protein type I receptor encoding DNA of 629 149 209 269 389 449 509 569 689 254 314 329 614 674 734 794 374 434 494 554 89 CAAGGATTCACCAAAAGCCCAGCTACGCAGGACAATAGAATGTTGTTGTCGGACCAATTTGTG AGCACCAGAGGACACCTTACCTTTCTAAAATGCTATTGCTCAGGACACTGCCCAGATGA CGCTATTAATAACACATGCATAACTAATGGCCATTGCTTTGCCATTATAGAAGAAGATGA rcaeceaeaaaccacerraacrrcreegrerareaagrareaaegcrerearrircaare CAACCAATATTTGCAGCCTACACTGCCCCTGTCGTTATAGGCCCATTCTTTGATGGCAG CAACCAATATTTGCAGCCTACACTGCCCCTGTCGTTATAGGCCCATTCTTGATGGCAG CGTCCGATGGCTGGCTGTCCATCTCTATGGCTGTCTGTATTGTCGCCATGATCGTCTT CTCCAGCTGCTTCTGTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA CTCCAGCTGCTTCTGTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGGTCGTTACAA TGGCCCGGACAGGACACGTGCGAATTGGACAATGACTCAGCTATACACTTACATT ACTGGGAGCCTGTCTCATCATTTCTCATGTTCAAGGGCAGAATCTAGATAGTATGCT ACTGGGAGCCTGTCTGTTCATTTCTCATGTTCAAGGGCAGAATCTAGATGGTATGCT CCATGGTACTGGTATGAAATCAGACGTGGACCAGAAGAAGCCGGAAAATGGAGTGACGTT TCAGGGAGAAACCACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG CAAGGATTCACCAAAAGCCCAGCTACGCAGGACAATAGAATGTTGTCGGACCAATTTGTG 30 TGCGGCCGCCAGGACACGTGCGAATTGGACAATGACTCAGCTATACACTTACATCAGATT AGCACCAGAGGACACCTTACCTTTAAAATGCTATTGCTCAGGACACTGCCCAGATGA CGCTATTAATAACACATGCATAACTAATGGCCATTGCCTTTGCCATTATAGAAGATGA Gaps Length 3167; 5 Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other; 6; Indels DB 14; Score 1750.4; Pred. No. 0; 0; Mismatches

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The invention relates to a novel isolated antibody, or its antigen-
binding fragment, which binds specifically to a sclerostin (SOST)
CC binding fragment, which binds specifically to a sclerostin (SOST)
CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
Cr 213 amino acids, fully defined in the specification (ADX97341,
CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
CC competitively inhibite binding of the SOST polypeptide to a bone
CC capable of binding site, where the BMP Type I Receptor binding site and a BMP Type I
Receptor binding site, where the BMP Type I Receptor binding site is
CC capable of binding to a BMP Type I Receptor binding site is
CC capable of binding to a BMP Type I Receptor binding site is
CC capable of standing to a BMP Type I Receptor polypeptide. The invention
C further comprises: a hybridoma cell producing the new antibody; a host
CC comprising the new antibody, or its antigen-binding fragment, and a
CC comprising the new antibody or its antigon-binding perture amino acids of
CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC 6, 9, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC 6 antibody and compositions are useful accids may be used in gene thersapy. The composition and methods are useful
CC for increasing bone mineralization, which may treat or prevent diseases
CC for increasing bone mineralization, which may treat or prevent diseases
CC conditions associated with low bone mineral density, such as
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                                                                                                                                                                                                                                                                                                                      antibody; sclerostin; SOST; bone morphogenic protein receptor;
Transforming Growth Factor; osteopathic; gene therapy; bone repair;
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                      1934 TCACAGGCTGCTAACAGTAAA-CTTTCAGGACTCTGCAGAATGC 1976
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mALK-3; activin receptor-like kinase; therapy; activin; TGF-beta; cancer; fibrosis; liver cirrhosis; pulmonary fibrosis; glomerulonephritis; mouse; rheumatoid arthritis; detection; diagnosis; drug screening; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel human and murine activin receptor-like kinases (ALK's). The novel ALK products can be used in therapy, e.g. to modulate conditions associated with activin or TGF-beta activity, such as fibrosis, e.g. liver cirrhosis and pulmonary fibrosis, cancer, rheumatoid arthritis and glomerulonephritis. The products can also be used for detection, diagnosis and drug screening. This sequence encodes the murine mALK-3 protein isolated from clones ME-7 and ME-D
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Matches 1678; Conservative
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receptor kinases identified as activin receptor like kinases (Alks) that are members of the transforming growth factor beta (TGF-beta) superfamily. The present invention describes a method for identifying TGF-beta inhibitors by determining whether a substance inhibite binding of TGF-beta to Alk-1, in particular where that substance is an antibody that binds to TGF-beta or the extracellular domain of Alk-1. The proteins having specific serine/ threonine receptor kinase activity can be used in therapy to modulate activin or TGF-beta activity and as such can be used to treat liver cirrhosis and pulmonary fibrosis, cancer, rheumatoid arthritis or glomenilonephritis. Accordingly, they exhibit hepatotropic, antiinflammatory, respiratory-Gen, cytostatic, antirheumatic, antiarthritic and nephrotropic activities. This polynucleotide is the murine ALK CDNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alk-1
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AAQ66640 standard; cDNA; 2070

RESULT 10 AAQ66640 AAQ66640

RXB

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The inventors have identified a new family of receptor kinases called activin receptor-like kinases (ALK). Their discovery was based on the realisation that receptor serine/threonine kinases form a new receptor family, which may include the type II receptors for other proteins in the transforming growth factor(TGF) beta superfamily. The activin receptor type II sequences from muuse and the dafi gene product of C.elegans have high sequence similarity and were used to design degenerate primers to clone related cDNA's (see AAQ66643-49). Six distinct putative receptor serine/threonine kinases (ALK 1.5, 4, and 6 are AAQ66639-42 respectively) are identified chalk.3 was obtained from a mouse lambdaEX lox cDNA ilbrary using hALK-3 cold a probe. Two overlapping clones were identified that together covered the complete sequence of mALK-3. CP Products of the invention can be used in therapy, ey. to modulate conditions associated with activin or TGF beta activity. These conditions include fibrosis, eg. liver cirrhosis and pulmonary fibrosis, cancer, theumatoid arthritis and glomeronephritis. (Updated on 25-MAR-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activin receptor-like kinase(s) with serine/threonine kinase domains have activin/TGF beta-type I receptor function and can be used in diagnosis or therapy or rheumatoid arthritis, glomerular nephritis, fibrosis, etc.
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                                                                                   serine threonine kinases; activin receptors; Act-R; superfamily; transforming growth factor; TGF; diagnostics; detection; therapy; rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
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                                                          Mouse Activin receptor-like kinase 3 (mALK-3) cDNA
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 94.1%;
Matches 1677; Conservative
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                                                                                                                                                                          New bone morphogenetic protein receptor kinase protein - used for identifying cpds. capable of binding it and for developing therapeutic cpds. and detection {\rm system}(s).
                                                                                                                                                                                                                                                   A cDNA library prepared from NIH3T3 poly-A RNA was screened with J159 fragment to isolate clone BRK-1 (sequence given in AAQ90184) encoding full-length BNP receptor kinase protein (AAR74343). Vectors including DNA were used to express recombinant BRK-1 in CHO and COS-7 hosts. (Updated on 25-MAR-2003 to correct PN field.)
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Pred. No. 0;
0; Mismatches 93; Indels 9;
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Best Local Similarity 94.2%;
Matches 1669; Conservative 0
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P-PSDB; AAR74343.
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TGGAATAGGATGTTGACTTGGTTTCCAGACTCCTTCTA-CATCTTCACAGGCTGCTA 1739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence encodes mouse bone morphogenetic protein (BMP) receptor type -I kinase-1 (BRK-1), which induces cellular differentiation in response -I bare gene may be inserted in plasmid pJT4, to form plasmid pJT4-J159F, and co-expressed with a type-II BRK-3 gene to study complex formation between the 2 receptor types. The BRK-3 receptor and antibodies against it may be used in diagnostic assays for BMP disorders, or in therapy to bind or scavenge BMPe. In addition, expression of the BRK-3 gene along with a reporter gene under the control of a hormone-responsive element in a cell culture may be used to screen compounds for BRK-agonist or -antagonist activity, by monitoring reporter gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated bone morphogenic protein receptor kinase protein - used to determine if a test cpd. is capable of binding to, or is (ant) agonist of BMP receptor kinase protein transcription.
                                                                                                                                                                                                                                                                                                                                                                                               "Bone morphogenetic protein receptor kinase-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GAATTGGACAATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGTCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bone morphogenetic protein receptor kinase-3; antibody; diagnostic; bone disorder; osteogenic; bone morphogenetic protein-agonist; drug screening, reporter gene; bone morphogenetic protein-antagonist; hormone-responsive element; ds.
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                                                                                                                                                                                                                                      bone morphogenetic protein receptor kinase-1;
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0; Mismatches
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Matches 1669; Conservative
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A cDNA clone (AAT28021) codes for full-length mouse bone morphogenetic protein (BMP) type I receptor kinase protein-1 (BRK-1) (AAR95225), a receptor capable of binding BMP and transducing a signal initiated by the binding. Host cells co-transfected with vectors carrying full-length, incomplete or soluble BMP type I receptor kinase protein cDNA and full-length, incomplete, soluble or truncated BMP type II receptor kinase protein-3 (BRK-3) cDNA (see also AAT28018-20 and AAT28022-30) express a BMP receptor complex useful for screening cpds. for BMP receptor affinity or for determining the concentration of a BMP receptor ligand in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      711 TAGTGGATCTGGATTACCTTTATTGGTTCAGCGAACTATTGCCAAACAGATTCAGATGGT 770
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                                                                                             Assays for bone morphogenetic protein activities – using complex of Bl
type I receptor kinase protein and BMP receptor kinase protein BRK-3.
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Matches 1669; Conservative
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                                                                                                                                                                                        TTACAACATGGTGCCTAGTGACCCATCTTATGAAGACATGCGTGAGGTCGTGTGTGAA
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                                              CTTGAACACCAGGGTGGGCACCAGGCGGTACATGGCTCCAGAAGTGCTGGACGAGACCCT
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BMP type I receptor kinase; BRK-1; BMP receptor; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA encodes a mouse BMP receptor kinase protein (BRK)-1. This can be used in the method of the invention of determining whether a compound can bind to a bone morphogenetic protein (BMP) receptor kinase protein complex. The method comprises allowing a compound in a sample to bind to the complex, where the complex is comprised of (i) a BMP; (ii) a BRK protein; (iii) an ActRIBE receptor. The method can be used to determine the concentration of a BMP receptor ligand in a sample by comparing the binding to a standard curve prepared with known concentrations of BMP ligand. The method can also be used to determine whether a test compound produces a signal on binding to a BMP receptor protein complex. The method is useful for determining whether a ligand, such as a known or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening method using bone morphogenetic protein receptor complex - which binds to potential drugs, and ActRIIB receptor used in the complex, also host cells transfected with DNA encoding the complex.
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                                                                               receptor kinase; ActRIIB receptor;
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Mouse BMP receptor kinase protein (BRK)-1 encoding cDNA.
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0y 1311 GAGTAAAACCATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTTGATCAT 1370 1261 GAATAAAACCATTTCCAGCCCTACATCATGACGACAACTTTGGTTTGATCATTTACATTACATTACATTACCATA 1320 0y 1371 TTGGGAGATGCGTGGTTGATTACAGAGGAATGCTGGAGGAATTACATTACCATA 1380 1321 TTGGGAATGGCTGGTGTGTTGATTACAGAGGAATGCGTGGAGAATACCATTACCATA 1380 0y 1431 TTACAACATGGTGGTGTGTTGATTACAGAGGAATGCGTGGAGATTACCATTACCATA 1380 0y 1411 TTACAACATGGTGCCTGTTACTACGGTGAACATGCGTGAGATTACCATTACCATA 140 0y 1181 TTACAACATGGTGCCCATTCAACGGTGAACAGGTGGTGTGTGAA 140 0y 1181 TACAACATGGTGCCCATTCAACGGTGAACAGGTGGTGTGAATTTTTTTT	RESULT 15 AAQ90183 ID AAQ90183 ID AAQ90183 ID AAQ90183 standard; DNA; 2056 BP. AC AAQ90183; XX AAQ90183; XX DT 25-MAR-2003 (revised) DT O1-NOV-1995 (first entry) XX
121 AGACTTGGACCAGAAGATGCTGCCCGAATGACCCCGAGGATACCTTGCC 180 111	771 TCGGCAGGTTGGTAAGGCCCGGTATGGAAGGTAGGATGGGTAAATGGCGTGAAAA 830 721 TCGGCAGGTTGGTAAGGCCCGTATGGAGAGTATGGATGGGTAAATGGCGTGGTGAAAA 780 721 TCGGCAGGTTGGTAAAGGCCCGTATGGAGAGTAAATGGCGTGGTGAAAA 780 831 AGTGGCTGCAAAGTATTTTTACCACTGAGAAACTAGATTAAAGGAAACAGAAAT 840 891 CTACCAGACGGTGTTATTTTACCACTGAGAAATAGCTTAAGGAAACAGAAAT 840 892 CTACCAGACGGTGTTAATGCGTCATGAAATTACTTGGTTTTATAGCTGCAGACATTAA 950 893 CTACCAGACGGTGTTAATGCGTCATGAAAATAACTTGGTTTTATAGCTGCAGACATTAA 950 894 CTACCAGACGGTGTTAATGCGTCATGAAAATAACTTGGTTTATAAGCTGCAGACATTAA 900 951 AGGCACTGGAACTCCTGGAAATTTTTGATTACTGATTACCATGAAAATGGGTCTCT 1010 901 AGGCACTGGTTCCTGGACTCAGCTGTATTTGATTACTGATTACCATGAAAATGGGTCTCT 1010 902 AGGCACTGGTTCCTGGACTCAGCTGTATTTGATTACTGATTACCATGAAAATGGGTCTCT 1010 903 AGGCACTGGTTCCTGGACTCAGCTGTATTTGATTACTGATTACCATGAAAATGGGTTTTTTC 1020 1011 CTATGACTGCTGTAATTGATTTTGATTACTGATTACCATGAAAATGGTTTTTTC 1020 1021 TGCTGCCTGGAACTGCCACTAGAAAATTATTGATTATAGGTACCCAAGGGAAGCTTTTTTTC 1020 1021 TGCTGCCTGTGGTCTGCCACCACAGAAAATTATTGGTACCCAAGGGAAGCTTGCTG 1130 1021 TATTGCTGAACTGCCACCACAAAAAAATTATAGGTACCCAAGGGAAGCTTGCTG 1130 1031 AATTGCTTGAGCCTAGCTGAAAAAAATTATAGGTACCCAAGGGAAGCTTGCTG 1140 1131 AATTGCTTGAGCCTAGCTGAAAAAAAATTATAAGAAAAATGGTAACAAGGAAGCTTGCTG 1140 1131 TATTGCTTGACCTGAAAAAAAAAAAAAAAAATTAAAAAAAA

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                                                                                              PCR primers (given in AAQ90186-89) based on unique sequences present in activin and DaF-1 receptor kinase domain VI were used to amplify cDNA derived from NIH3T3 cells. A 3100 bp PCR fragment obtd. was used to screen a cDNA library prepd. From NIH3T3 cells in lambda ZapII to obtain clone 159 contaning DNA (AAQ90183) encoding truncated BRK-1 (AAR74342). Vectors including the DNA were used to express recombinant tBRK-1 in CHO and COS-7 hosts. (Updated on 25-MAR-2003 to correct PN field.)
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Pred. No. 0;
                                                                                                                                                                                                                                0; Mismatches
                                                                            English
                              New bone morphogenetic protein identifying cpds. capable of bicpds. and detection system(s).
                                                                                                                                                                                                         78.6%;
llarity 90.3%;
Conservative
                                                                       Claim 6; Page 25-28; 49pp;
1995-206935/27
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Best Local Similarity
Matches 1584; Conserv
WPI; 1995-206935/
P-PSDB; AAR74342.
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Search completed: December 9, 2005, 14:08:06 Job time: 775 secs

Carried March Control

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17, Appl 7, Appli 17, Appli 3, Appli 3, Appli 3, Appli 4525, Ap

Sequence Seq

Run on:

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MEDIUM TYPE: Floppy disk
COMPUTER: END FOCOMPALISE
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COMPUTER: END FOCOMPALISE
CORERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-SEP-1993
CLASSIFICATION STANDIN: SAO
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEFOND: 617 876 1170
TELEFOND: 617 876 1170
TELEFOND: 617 876 5551
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: MULDEL CALL STANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    B: Genetics Institute Inc.- Legal Affairs
87 CambridgePark Drive
         US-09-382-256-17
US-09-395-115-17
US-09-436-115-17
US-09-446-171A-7
US-09-267-963D-17
US-09-267-963D-17
US-09-267-963D-17
US-08-123-934A-3
US-08-949-016-4525
US-08-949-016-4525
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US-08-462-467B-19
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US-09-382-256-7
                                                                                                                                                                                                                                                      ALIGNMENTS
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APPLICANT: CELESTE, Anthony J.
APPLICANT: THIES, R. SCOLT
TITLE OF INVENTY YAMAJI, NO. 62912060TU
TITLE OF INVENTYON: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Le
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/08123934A; Patent No. 6291206; GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
INMEDIATE SOURCE:
CLONE: CFK1-23a
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Sequence 1, Appli
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Sequence 604, App
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                                                                       December 9, 2005, 13:41:38; Search time 247 Seconds (without alignments)
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US-09-874-628-1
; Sequence 1, Application US/09874628
; Patent NO. 6610513
; GENERAL INFORMATION:
; GELESTE, Anthony J.
THIES, R. SCOTT
YAMAJI, NO. 66105130ru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affers STREET: 87 Cambridge
; STREET: 87 Cambridge
; STREET: MA
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                                                        CTAGTGGATCCCCCGGGCTGCAGGATTCTGCGGCCGCCAGGACACGTGCGAATTGGACA
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                                             CTAGTGGATCCCCCGGGCTGCAGGAATTCTGCGGCCGCCAGGACACGTGCGAATTGGACA
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                            Gaps
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        Length 1813
                           Indels
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       b; Score 1813; I
b; Pred. No. 0;
0; Mismatches
       Query Match
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Matches 1813; Conservative 0
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                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/874,628
FILING DATE: 05-Jun-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,934
FILING DATE: 17-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1813;
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEFAX: 617 876 1170
TELEGTH: 1813 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
                ZIP: 02140
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 1813; Conserv
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Db 1561 TCAGAATGCTGGGCCCATAATCCAGCATCCAGACTCACAGCTTTGAGAATCAAGAAGACG 1620 Qy 1621 CTCGCAAAGATGGTTGAATCCCAGGATGTAAAGATTTGACAAACAGTTTTGAGAAAGAA	QY 1681 TTAGACTGCAAGAAATTCACCCGAGGAGGGGGGGGTTAGCATGGACTACGATGTCGGCT 1740	1741 TGGTTTCCAGACTCTCCTCTACCATCTTCACAGGCTGCTAACAGTAAAACCTTTCAGGA	0y 1801 CTCTGCAGAATGC 1813 	RESULT 3 PCT-US94-10080-1 . Carried 1 Annliation DC/WIGG410080	GENERAL INFORMATION: APPLICANT: GENETICS INSTITUTE, INC. TITLE OF INVENTION: RECEPTOR PROTEINS ATMADED OF CONTENTS: 1	CORRESPONDENCE ADDRESS: ; ADDRESSEE: Genetics Institute Inc Legal Affairs ; STREET: 87 CambridgePark Drive	STATE: MA STATE: MA COUNTRY: USA COUNTRY: USA STATE: MA COUNTRY:		SUBJECT OF STATEMENT RELEASE #1.0, VETSION #1.25 CURRENT APPLICATION DATA: PILING DATE: HEREWITH	CLASSIFICATION DATA: PELLOR DATE: 17-SEP-1993	Ψ	; TELEPEANUS (617) 498-8260; TELEPAN C617) 498-8260; TELEPAN C617) 498-8260; TELEPAN C617) 400-8260	FORTING SECTION SECTIO	SIGNAL BANDLESS: BINGLE TOPOLOGY: TOPOLOGY: BINGLE MOLECULE TYPE: DNA (genomic) IMMEDIATE SOURCE:	; FEATURE: CENT.23a; FEATURE:; NAME/KEY: CDS ; NAME/KEY: CDS ; NAME/ACTION: 611656	100.0%; Score 1813; DB 6; Length 1813;	vacive 0; cccccgggcrgcac

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                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 930460.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: AUJLY 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: AUJLY 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: AUGUST 3, 1993
APPLICATION NUMBER: 931344.5
FILING DATE: October 15, 1993
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: NO. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
TELEFRX: (212) 318-3000
TELEFRX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: CDNA
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 87.2%; Score 1581.4; Best Local Similarity 94.1%; Pred. No. 0; Matches 1678; Conservative 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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ANTI-SENSE: NO
FRAGMENT TYPE: int
ORIGINAL SOURCE:
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                                                                                               CTGGGCCTAGCTGTTAAATTCAACAGTGACACAATGAAGTTGACATACCCTTGAACAC
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FRANZEN, Peter
FRANZEN, Peta
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVUIN RECEPTOR LIKE KINASES,
AND THEIR USE
AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUMRY: USA
ZIP: 10103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09382256A Patent No. 6207814 GENERAL INFORMATION:
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RESULT 5

US-09-395-115-13

Sequence 13, Application US/09395115

Sequence 13, Application US/09395115

Sequence 13, Application US/09395115

GENERAL INFORMATION:

APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;

APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins

TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their INUMBER OF SEQUENCES:

NUMBER OF SEQUENCES:

CORRESPONDENCES:

ADDRESSEE: Felle & Lynch

STREET: 805 Third Avenue
                                                                                                                            TCGAGCAGTTTTGAAGCTAATGTCAGAATGTTGGGCCCCATAATCCAGCCTCCAGACTCAC
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TCAATTACCATATTACAACATGGTGCCCAGTGACCATCCTATGAGGACATGCGTGAGGT
                                               CGTGTGTGTGTGAAACGCTTGCGGCCAATCGTCTCTAACCGCTGGAACAGTGATGAATGTCT
                                                                 TCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCCATAATCCAGCATCCAGACTCAC
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/436,265
PILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6271365ember-1993
APPLICATION DATA:
PLING DATE: 17-No. 6271365ember-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
PLING DATE: 8-March-1993
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/395,115
FILING DATE:
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APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 9304680.3 FILING DATE: 8-March-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Felfe & Lynch
STRET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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                                                                                                                                              TTTGCAGCCTACACACCCCCCTGTTGTTATAGGTCCGTTCTTTGATGGCAGCATCCGATG
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                      AACCACATTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC
                                                               ACCAAAAGCCCCAGCTACGCAGGACAATAGAATGTTGTCGGACCAATTTTGTGCAACCAATA
                                                                                                                            TITICAGCCTACACTGCCCCCTGTCGTTATAGGCCCCATTCTTTGATGGCAGCGTCCGATG
                                                                                                                                                                                       GCTGGCTGTGCTCATCTCTATGGCTGTCTGTATTGTCGCCATGATCGTCTTCTCCAGCTG
                                                                                                                                                                                                                                                  CTTCTGTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAACCGTGACTT
                                                                                                                                                                                                                                                                                                               GGAACAGGATGAAGCATTTATTCCAGTAGGAGAATCACTGAAAGACCTGATTGACCAGTC
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87.2%; Score 1581.4;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1678; Conservative 0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
RADOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOAlei, Vineet
REGISTRATION NUMBER: 37,003
REGISTRATION NUMBER: 37,003
REGISTRATION NUMBER: 17,003
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
REGISTRATION: 1000
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; LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAACACATGCATAACTAATGGCCATTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGA 338
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                                                                                                                                                       87.2%; Score 1581.4;
94.1%; Pred. No. 0;
cive 0; Mismatches
                                                                                                                                                     Query Match
Best Local Similarity 94.1
Matches 1678; Conservative
                internal
ANTI-SENSE: NO
FRAGMENT TYPE: into
ORIGINAL SOURCE:
ORGANISM: Mouse
                                                                                    NAME/KEY:
LOCATION:
                                                                                                          ; LOCATION:
US-08-436-265-13
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                       APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                    1934 CACAGGCTGCTAACAGTAAACCTTACCGTACTCTACAGAATAC 1976
                                                                1771 CACAGGCTGCTAACAGTAAACCTTTCAGGACTCTGCAGAATGC 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                          kb storage
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APPLICATION D443
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION DATA: 9304680.3
FILING DATE: 8-March-1993
APPLICATION NUMBER: 931047.6
FILING DATE: 2-May-1993
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION NUMBER: 913609.2
FILING DATE: 3-August-1993
PRIOR APPLICATION NUMBER: 913609.2
FILING DATE: 3-August-1993
PRIOR APPLICATION NUMBER: 913609.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette, 3.5 inch, 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
CLASSIFICATION: 435
                                                                                                                                                                                        Sequence 13, Application US/08436265
Patent No. 6316217
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 9321344.5 FILING DATE: 15-October-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM
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CTGTCTGTTCATCATTTCTCATGTTCAAGGGCAGAATCTAGATAGTATGCTCCCATGGTAC 158
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                                                                                 ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                 PFILING DATE: 03-000
PFILING DATE: 03-000
PFILING DATE: 03-000
PFILING DATE: 03-0000
PFILING DATE: 03-000
PFILING DATE: 03-0000
PFILING DATE: 03-000000
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94.1%; Pred. No. 0;
iive 0; Mismatches
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REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        SOFTWARE: Wordperfect
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-OCT-2000
: 805 Third Avenue
New York City
                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS
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TYPE: nucleic acid
STRANDEDNESS: unknown
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Best Local Similarity 94.1
Matches 1678; Conservative
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ORIGINAL SOURCE:
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ANTI-SENSE: NO
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US-09-679-187-13
                           CITY: N
STATE:
ZIP: 10
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                           1095 TGCAGACATTAAAGGCACTGGTTCCTGGACTCAGCTGTATTTGATTACTGATTACCATGA 1154
                                                                                                                                             1059 GTTAGCTTATTCTGCTGCCTGTGGTCTGTGCCACCTCCACACAGAAATTTATGGCACGCA 1118
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Sequence 13, Application US/09679187

Sequence 13, Application US/09679187

Sequence 10. 6331621

GENERAL INFORMATION:

APPLICANT: Miyazono, Kohei, Dijke, Peter Ten;

APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik

APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik

TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins

TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch
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               AGTIGACATACCCTIGAACACCAGGGIGGCCACCAGGCGGTACATGGCTCCAGAAGTGCT
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CTGTCTGTTCATCTTCTCATGTTCAAGGGCAGAATCTAGATAGTATGCTCCATGGCAC 314
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                                            GGACACCTTACCTTAAAATGCTATTGCTCAGGACACTGCCCAGATGACGCTATTAA
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                        TGGTATGAAATCAGACGTGGACCAGAAGAGCCGGAAAATGGAGTGACGTTAGCACCAGA
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Sequence 13, Application US/09267963D

Sequence 13, Application US/09267963D

Patent No. 6692925

GENERAL INFORMATION:
APPLICANT: MYAZONO, Kohei
APPLICANT: MAWURA, Takeshe
APPLICANT: MAWURA, Takeshe
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE
TITLE OF INVENTION: NUMBER: US/09/267, 963D
CURRENT APPLICATION NUMBER: US/09/267, 963D

CURRENT APPLICATION NUMBER: US/09/267, 963D

PRIOR APPLICATION NUMBER: US/09/267, 963D

PRIOR APPLICATION NUMBER: US/09/317

PRIOR APPLICATION NUMBER: US/039,177

PRIOR APPLICATION NUMBER: US/039,177

PRIOR APPLICATION NUMBER: US/039,177

SEQOID NOS: 46

SOFTWARE: Patent In version 3.2

LENGEN APPLICATION OF SECOID NOS: 46

SECOID NO 0.3 8 CAGGACACGTGCGAATTGGACAATGGCTCAGCTATACACTTACATCAGATTACTGGGAGC Length 2070; 6 DB 3; 96; 87.2%; Score 1581.4; 94.1%; Pred. No. 0; iive 0; Mismatches

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US-08-4678-11

US-08-467-11

Sequence 11. Application US/08462467B

Sequence 11. Application US/08462467B

Sequence 11. Application US/08462467B

Sequence 11. Application US/08961

GENERAL INFORMATION:
TITLE OF INVENTION: The Use of a BMP Protein Receptor
TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells
TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells
TITLE OF INVENTION: BMP Receptor
TITLE OF INVENTION: BMP Receptor
TITLE OF INVENTION: BMP Receptor
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Procter & Gamble Company
STREET: 11810 East Miami River Road
CITY: Ross
STATE: OH

COUNTRY: USA
                                                                                                                                             GGACGAGAGCCTGAGTAAAACCATTTCCAGCCCTACATGGCTGACATCTACAGCTT
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                                                       AGTTGACATACCCTTGAACACCCAGGGTGGGCACCAGGCGGTACATGGCTCCAGAAGTGCT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,467B
FILING DATE:
CLASSIFICATION: 415
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                                                                                                                                                                                              Score 1574.2;
Pred. No. 0;
0; Mismatches
      NAME: Hereko, Bart S.
REGISTRATION NUMBER: 32,572
REFERENCE/DOCKET NUMBER: 5474R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-0630
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2402 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 94.2%;
Matches 1669; Conservative
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                                                              RECEPTOR
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                                                                                                                                              COUNTRY: USA
ZIP: 45061
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,735A
FILING DATE: 24-NOV-1993
CLASSIFICATION: 435
ATTOMEY/AGENT INFORMATION:
NAME: CORSTANIE, BRAHM J.
REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 5088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-0260
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2402 base pairs
                                                              A BMP
                                                             FOR
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Pred. No. 0;
0; Mismatches
                                                                                               :: THE PROCTER & GAMBLE COMPANY 11810 EAST MIAMI RIVER ROAD
                                                            CODING
APPLICANT: COOK, JONATHAN S.
APPLICANT: KOENEA, PAUL E.
APPLICANT: KOENIG, BETH B.
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: TING, JERRY
TITLE OF INVENTION: DNA SEQUENCE CO
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER & GAMBLE C.
ADDRESSEE: THE PROCTER & GAMBLE C.
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join(11..1606)
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Best Local Similarity 94.2'
Matches 1669; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
                                                                                                                   CITY: ROSS
STATE: OH
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                    , NAME/KEY:
, LOCATION:
US-08-158-735A-3
                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: NOHNO, TSUTOWU
TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
STREET: 11810 EAST MIAMI RIVER ROAD
CITY: ROSS
STATE: OH
COUNTRY: US
ZIP: 45061
COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PATENTIN Release #1.30, Version #1.30
COMPUTER: DATE: OH-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.30, Version #1.30
CURRESTORMENT APPLICATION DATA:
APPLICATION NUMBER: 34,004
FLING DATE: OH-NOV-1994
CLASSIFICATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 5473
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 11:
SEQUENCE CARAACTERISTICS:
LENGTH: 2402 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: CDOLOGY: linear
MOLECULE TYPE: CDNA
FRANTIRE:
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                        RESULT 11
US-08-334-179A-11
; Sequence 11, Application US/08334179A
; Patent No. 6306622
; GENERAL INFORMATION:
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Best Local Similarity 94.2%;
Matches 1669; Conservative
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; LOCATION: join
US-08-334-179A-11
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                                                                                                                                                                                                                                                                         Query Match 78.6%; Score 1424.4; Best Local Similarity 90.3%; Pred. No. 0; Matches 1584; Conservative 0; Mismatches
REGISTRATION NUMBER: 34,804
REFERIOR/DOCKET NUMBER: 5088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-2858
TELEFAX: (513) 627-2056
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2056 base pairs
TYPE: mullelc acid
STRANDEDNESS: double
                                                                                                                                                                                                                          join(291..1790)
                                                                                                                                                                                                          CDS
                                                                                                                                                                                                       ; NAME/KEY;
; LOCATION;
US-08-158-735A-1
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APPLICANT: CORREA, PAUL E.
APPLICANT: CORRIG, BETH B.
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: TING, JERRY
TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 45061
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,735A
FILING DATE: 24-NOV-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: THE PROCTER & GAMBLE COMPANY
STREET: 11810 EAST MIAMI RIVER ROAD
CITY: ROSS
STATE: OH
COUNTRY: USA
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NAME: CORSTANJE, BRAHM J.
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US-08-158-735A-1
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 APPLICANT: TEN DIJKE, Peter
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohei
APPLICANT: MIYAZONO, Kohei
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor NUMBER OF SEQUENCES: 18
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,337A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MEYERS, Thomas C.

REGISTRATION NUMBER: 36,989

REFRENCE/DOCKET NUMBER: 36,989

REFRENCE/DOCKET NUMBER: 36,989

REFRENCE/DOCKET NUMBER: CRP-097CP2

TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LCCATION: 310..1905
; OTHER INFORMATION: /product= "Human ALK3"
US-08-481-337A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2932 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                   CITY: Boston
STATE: MA
COUNTRY: USA
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588 AACCACATTAGCTTCAGGGTGTATGAAATATGAAGGATCTGATTTTCAGTGCAAAGATTC

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Sequence 5, Application US/08481337A; Patent No. 5863738; GENERAL INFORMATION:

US-08-481-337A-5

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                                                                     GAATGGGTCTCTATGACTTCCTGAAATGTGCCACCCTGGACACCAGAGCCCTACTCAA
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NAME/KEY: CDS
LOCATION: 310..1905
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                       ORGANISM: Homo sapiens
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                                        Sequence 5, Application US/09395115;
Patent No. 6271365;
Patent No. 6271200;
Patent No
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APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-OCCOBE-1995
APPLICATION NUMBER: PCT/CB93/02367
FILING DATE: 17-No. 6271365ember-1993
APPLICATION NUMBER: PCT/CB93/02367
FILING DATE: 17-No. 6271365ember-1993
APPLICATION DATA: 4PPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 931363.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-OCCOBE-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-OCCOBE-1993
ATTORNEY/AGENT INFORMATION: NUMBER: N
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/395,115
FILING DATE:
CLASSIFICATION:
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REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
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INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2932 base pairs TYPE: nucleic acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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LOCATION:
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                                       CGGCCTAATCATTTGGGAGATGGCTCGTCGTTGTATCACAGGAGGATCGTGGAAGAATA
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                                                         TGGTTTGATTTTGGGAGAGAGGCCCCTGTATTACAGGAGGAATCGTGGAGGAATA
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Search completed: December 9, 2005, 17:20:36 Job time : 255 secs

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
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MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
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STRANDEDNESS: single
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COUNTRY: USA
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Sequence 89, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 116, Appl
Sequence 116, Appl
Sequence 85, Appli
Sequence 85, Appli
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Sequence 90, Appl
Sequence 119, App
Sequence 120, App
Sequence 88, Appl
                                                                                  (without alignments)
14485.394 Million cell updates/sec
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Sequence 5, Appli
Sequence 1, Appli
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Sequence 121, App
Sequence 90, Appl
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Sequence 307,
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1813
1 CTAGTGGATCCCCCGGGCTG......TTCAGGACTCTGCAGAATGC 1813
                                                                    December 9, 2005, 15:52:22 ; Search time 1035 Seconds
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/ cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-450-763-22861
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US-10-153-217-1
US-10-745-237-307
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US-10-600-645-1

US-10-463-190-121

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US-10-463-190-119

US-10-68-497-89

US-10-868-497-89

US-10-868-497-89

US-10-868-497-89

US-10-968-133-13

US-09-913-131-13

US-09-913-68-5

US-10-286-152A-37

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                                    CGAGACCTGAAGAGCAAAAACATCCTTATTAAGAAAAATGGTAGTTGCTGTATTGCTGAC
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GENERAL INFORMATION:
THIES, Anthony J.
THIES, R. SCOLT
MAMAIL OF INVENTION: RECEPTOR PRE NUMBER OF SEQUENCES: 19
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                                                                                                                     CCAGTAGGAGAATCACTGAAAGACCTGATTGACCAGTCACAAAGCTCTGGTAGTGGATCT
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                                             DB
                                           100.0%; Score 1813;
100.0%; Pred. No. 0;
ive 0; Mismatches
, NAME/KEY: CDS
; LOCATION: 61..1656
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-874-628-1
                                          Query Match
Best Local Similarity 100.
Matches 1813; Conservative
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/600,645
FILING DATE: 23-Jun-2003
CLASSIFCATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-SEP-1993
ATTORNEY/AGENT INFORMATION:
          Legal Affairs
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100.0%; Pred. No. 0;
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       ADDRESSEE: Genetics Institute I STREET: 87 CambridgePark Drive CITY: Cambridge STATE: MA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 61..1656
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                      NAME: LAZAR, SLEVEN R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEPHONE: 617 876 1170
TELEPAX: 617 876 1170
                                                                        ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
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Best Local Similarity 100.
Matches 1813; Conservative
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	RESULT 4 US-10-868-497-90 Sequence 90, Application US/10868497 Publication No. US20050106683A1 GENERAL INFORMATION: APPLICANT: Winkler, David G. APPLICANT: Winkler, David G. APPLICANT: Winkler, John TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION FILE REFERENCE: 60117-128 CURRENT APPLICATION NUMBER: US/10/868,497 CURRENT PILING DATE: 2004-06-15 NUMBER OF SEQ 1D NOS: 112 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ 1D NO 90 LENGTH: 3003 TYPE: DNA ORGANISM: Rattus norvegicus US-10-868-497-90	Query Match 96.5%; Score 1750.4; DB 9; Length 3003; Best Local Similarity 99.6%; Pred. No. 0; Actobactor Actobactor

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GCGTGAGGTCGTGTGTGAAACGCTTGCGGCCAATCGTCTCTAACCGCTGGAACAGTGA
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.larity 99.6%; Pred. No. 0;
.Conservative 0; Mismatches 6; Indels 2;
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US-10-463-190-119
i Sequence 119, Application US/10463190
i Publication No. US20040009535A1
i GENERAL INFORMATION:
i APPLICANT: BUTNKOW, Mary E.
i APPLICANT: Galas, David J.
i APPLICANT: Kovacevich, Brian
APPLICANT: Mulligan, John T.
i APPLICANT: Mulligan W.
i APPLICANT: Walligan W.
i APPLICANT: UNINKER. Bryan W.
i APPLICANT: Walligan W.
i APPLICANT: Walligan W.
i APPLICANT: Walkler, David G.
i TITLE OF INVENTION: COMPOSITION SAND MEHTODS
i TITLE OF INVENTION: LACENCE 240083.508C2
i CURRENT FILING DATE: 2003-06-16
i NUMBER OF SEQ ID NOS: 143
i SOFTWARE: FastSEQ for Windows Version 3.0
i SENGTH: 3167
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Best Local Similarity
Matches 1776; Conserv
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AGAAGTGCTGGACGAGGCCTGAGTAAAAACCATTTCCAGCCCTACATCATGGCTGACAT 1349
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                          GCGTGAGGTCGTGTGTGAAACGCTTGCGGCCAATCGTCTCTAACCGCTGGAACAGTGA
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AAAGATTTGACAAACAGTTTTGAGAAAGAATTTAGACTGCAAGAAATTCACCCGAGGAAG
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BONE MINERALIZATION
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US-10-668-497-88

Sequence 88, Application US/10868497
Publication No. US20050106683A1
GENERAL INFORMATION:
APPLICANT: Winkler, David G.
APPLICANT: Latham, John
TITLE OF INVENTION: METHODS FOR INCREASING BON;
FILE REFERENCE: 60117-128
CURRENT FILING DATE: 2004-06-15
CURRENT FILING DATE: 2004-06-15
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 88

SEQ ID NO 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1750.4;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.6%;
Matches 1776; Conservative
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; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-868-497-88
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APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-OCTOBER-1993
ATTORNAY AGENT INFORMATION:
NAME: KOAlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENGE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE GHARACTERISTICS:
LENGTH: 2010 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.2%; Scor.
94.1%; Pred. No. v,
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; EQUENCE DESCRIPTION: SEQ ID NO: 13: US-09-903-068-13
                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity ....
Matches 1678; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-like Kinase, Proteins
Having Serine Threonine Kinase Domains And Their Use
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 GCGTGAGGTCGTGTGTGTGAAACGCTTGCGGCCAATCGTCTCTAACCGCTGGAACAGTGA 1529
                                                                                                                                                                                                                                                                                         TGAATGTCTTCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCATAATCCAGCATC 1589
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                                                                                                                                                              GGAGGAATATCAATTACCATATTACAACATGGTGCCTAGTGACCCATCTTATGAAGACAT
                                                                                 CTACAGCTTTGGTTTGATCATTTGGGAGATGGCCCGTCGTCGTATTACAGGAGGAATCGT
                                                                                                                                                                                                                                                   1635 GCGTGAGGTCGTGTGTGAAACGCTTGCGGCCAATCGTCTTAACCGCTGGAACAGTGA
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPENATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/903,068
FILING DATE: 11-Jul-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. US20020123139Alember-1993
APPLICATION NUMBER: 9224057 1
FILING DATE: 17-No. US20020133139Alember-1992
FILING DATE: 17-No. US20020133139Alember-1992
FILING DATE: 9-March-1993
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9311047.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/679,187
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09903068
Patent No. US20020123139A1
GENERAL INFORMATION:
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US-09-903-068-13
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& g	759 GATTCAGATGGTTCGGCAGGTTGGTAAGGCCCGGTATGGAAGTATGGATGG	щo
රු දු	819 GCGTGGTGAAAAAGTGGCTGTCAAAGTATTTTTTACCACTGAAGAAGCTAGCT	; Publication No. US20050048607A1 ; GENERAL INFORMATION: ; APPLICANT: MIYAZONO, Kohei ; APPLICANT: IMAMURA, Takeshe
<u>ک</u> م	879 AGAAACAGAAATCTACCAGACGGTGTTAATGCGTCATGAAAATATACTTGGTTTTATAGC 938 	
රු පු	939 TGCAGACATTAAAGGCACCGGTTCCTGGACTCAGCTGTATTTGATTACTGATTACCATGA 998 	; CURRENT APPLICATION NUMBER: US/10/739,413 ; CURRENT FILING DATE: 2003-12-19 ; PRIOR APPLICATION NUMBER: US/09/267,963 ; PRIOR FILING DATE: 1999-03-12
දු දු	. 999 GAATGGGTCTCTATGACTTCCTGAAATGTGCCACCCTGGACACCCAGAGCCCTACTCAA 1058 	
ۇ <u>ۋ</u>	1059 GTTAGCTTATTCTGCTGCTGTGGTCTGTGCCACCTCCACACACA	; NUMBER OF SEQ ID NOS: 46 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 13 ; LENGTH: 2070
ò 8	1119 AGGCAAGCCTGCAATTGCTCATCGAGACCTGAAGAGCAAAAACATCCTTATTAAGAAAAA 1178 	
승 옵	1179 TGGTAGTTGCTGTATTGCTGACCTGGGCCTAGCTGTTAAATTCAACAGTGACACAAAATGA 1238 	Query Match 87.2%; Score 1581.4; DB 9; Length 2070; Best Local Similarity 94.1%; Pred. No. 0; Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;
දු පු		Oy 39 CAGGACACGTGCGAATTGGACAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC 98
<u>څ</u> ۾		Qy 99 CTGTCTGTTCATCATTTCTCATGTTCAAGGGCAGAATCTAGATAGTATGCTCCATGGTAC: 158
ć d	TGGTTTGATCATTTGGGAGATGGCCCGTGCTGTATTACAGGAGGAATCGTGGAGGAGTA 1	Qy 159 TGGTATGAAATCAGACGTGGACCAGAAGAGCGGAAAATGGAGTGACGTTAGCACCAGA 218
상 원	1419 TCAATTACCATATTACAACATGGTGCCTAGTGACCCCATCTTATGAAGACATGCGTGAGGT 1478 	Oy 219 GGACACCTTACCTTAAAATGCTCATTGCTCAGGACACTGCCCAGATGACGCTATTAA 278
දු පු		Qy 279 TAACACATGCATAACTAATGGCCATTGCCATTATAGAAGAAGATGATCAGGGAGA 338
9 9	7	339 AACCACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 39
6 8	1599 AGCTTTGAGAATCAAGAAGACGCTCGCAAAGATGGTTGAATCCCAGGATGTAAAGATTTG 1658 	Oy 399 ACCAAAAGCCCAGCTACGAGGACAATAGAATGTTGTGGACCAATTTGTGCAACCAATA 458
è d	1659 ACAAACAGTTTTGAGAAAGAATTTAGACTGCAAGAAATTCACCCGAGGAAGG 1710 	Oy 459 TTTGCAGCCTACACTGCCCTGTCGTTATAGGCCCATTCTTGATGGCAGCGTCCGATG 518

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Sequence 11, Application US/09742153
Publication No. US20030096296A1
GENERAL INFORMATION:
APPLICANT: Rosenbaum, Jan S
TITLE OF INVENTION: The Use of a BMP Protein Receptor
Complex for Screening Bone Metabolism Actives and Cell,
Co-Transfected With a Type II BMP Receptor and a Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATTICICATGITCAAGGGCAGAATCIAGATAGTAIGCICCATGGTACTGGTAIGAAATC 170
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----ACCCGAGGAAGG
                                                                                             GIGGAGTTAGCATGGACTAGGATGTCGGCTTGGTTTCCAGACTCTCTCCTCTACTTT
                                                                                                               GTGGGATTAGCATGGAATAGGATGTTGACTTGGTTTCCAGACTCCTTCTA-CATCTT
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                                                                                                                                                    CACAGGCTGCTAACAGTAAACCTTTCAGGACTCTGCAGAATGC 1813
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.30
                                           AC----AAACAGTTTTGAGAAAGAATTTAGACTGCAAGAAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93;
                                                                                                                                                                                                                                                                                                                                                                                           Gamble Company
River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Ver
ROFTWARE: Patentin Release #1.0, Ver
APPLICATION NUMBER: US/09/742,153
FILING DATE: 20-Dec-2000
CLASSIFICATION AUTHORNATION:
APPLICATION NUMBER: 08/462,467
FILING DATE: 05-UNN-1995
ATTORNEY/AGENT INCRNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.8%; Score 1574.2;
94.2%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Procter & Gamble STREET: 11810 East Miami River CITY: Ross
CITY: Ross
STATE: OH
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hersko, Bart S.
REGISTRATION NUMBER: 32,572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: (TELECOMMUNICATION: TELEPHONE: (513) 627-0633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (513) 627-0260
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2402 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 94.2
Matches 1669; Conservative
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AATC TACC TGCC TGCC TAAC TAAC	TCTGGGTGTATGAAGGCTCTGATTTCAATGCAAGGATTCACCGAAGAACTCTGGGGGGGG	481 CATTICCATGGCTGTGTATAGTTGTTATCATCTTCTCCAGCTGCTTTTGCTATAA 540 591 ACATTACTGTAAGAGTATCTCAAGCAGGGTGGTTACACCGTGACTTTGGAACAGGATGA 650 [1]	TCGCCAGGTTGGTAAGGGCCGGTATGGAGAAGTATGGATGG	1071 TGCTGCCTGTGCCACCTCCACACAGAGCCCTACTCAAGTTATC 1020 1071 TGCTGCCTGTGGCCACCTCCACACAGAAATTTATGGCACGCAAGCCTGC 1130 1071 TGCTGCCTGTGGCACCTCCACACAGAAATTTATGGTACCCAAGGGAAGCCTGC 1130 1131 AATTGCTCATCGAGACCTGAAGAAAAAATTTATGGTACCCAAGGGAAGCCTGC 1080 1131 AATTGCTCATCGAGACCTGAAGAAAAAATGTTATAAGAAAAATGGAAGTTGCTG 1190 1191 TATTGCTGACCTGGGCCTAGCTGTTAAAATCAACAGTGAAAAATGGAAAAATGCTGCTG 1140 1191 TATTGCTGACCTGGGCCTAGCTGTTAAATTCAACAGTGACACAAATGAAATACCTACC
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Qy 159 TGGTATGAAATCAGACGTGGACCAGAAGAGGCGGAAATGGAGTGACGTTAGCACCAGA 218 Db 389 TGGTATGAAATCAGACTTGGACCAGAAGAAGCCAGAAATGGAGTGACTTTAGCACCAGA 448 Qy 219 GGACACCTTACTTTAAAATGCTATTGCTCAGGACACTGCCCAGATGACGTATTAA 278 H	629 ACCGAAAGCCTACGCAGGACATAGAATGTTGTCGGACCAATTTGTGCAACCAGTA 459 TTTGCAGCCTACACTGCCCTGTCGTTATAGGCCCATTTTGATGGCAGCGTCCGATG 689 TTTGCAGCCTACACTGCCCCTGTTGTTGTTGTTCGTTGTTGATGGCAGCGTCCGATG 689 TTTGCAGCCTACACTGCCCCTGTTGTTTGTTGTTCGTTTTTTGATGGCAGCATCCGATG 519 GCTGGCTGTTCTATTGCTGTTTTTGTTGTTCGTTTCTCCCAGCTG 749 GCTGGTTGTTCTATTCTTTTCTTGTTATTGTTGTTGTTTTTTTT	Qy 639 GGAACAGGATGAAGCATTTATTCCAGTAGAGAATCACTGAAAGACCTGATTGACCAGTC 698 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 759 GATTCAGATGGTTCGGCAGGTTGGTAAGGGCCGGTATGGAAGTATGGATGG	Oy 999 GAATGGGTCTCTCTATGACTTCCTGAAATGTGCCACCTGGACACCAGAGCCCTACTCAA 1058 Db 1229 AAATGGATCTCTCTATGACTTCCTGAAATGTGCCACCTAGACACCAGAGCCCTACTCAA 1288 Oy 1059 GTTAGCTTATTCTGCTGCTTGTGCCACCTCCACACAGAAATTTATGGCACGA 1118 Db 1289 GTTAGCTTATTCTGCTGCTTGTGCCACCTCCACACACAAATTTATGGAACACACAAAATTTATGGAACACACAC

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Best Local Similarity 87.8%; Pred. No. 0;
Matches 1561; Conservative 0; Mismatches 205; Indels
                                                                                                                                                  MAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMUNICATION INFORMATION:
TELEFHONE: (212) 688-9200
TELEFFX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base paire
       FILING DATE: 8 MAICH-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 28 MAY-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-401y-1993
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-OCCODET-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 310..1905
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
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Qy 1659 ACAAACAGTTTTGAGAAAGAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1709 Db 1908 ATGGTTAAACCATCGGAGAAACTCTAGACTGCAACAACTGTTTTTACCCATGGCATG 1967 Qy 1710 GGTGGAGTTAGCATGGACT-AGGATGTCGGCTTGGTTTCCAGACTCTCTCCTC-TACCAT 1767 Db 1968 GGTGGAATTAGAGTGGAATAACTTGGTTCTCAGACTCTTTCTCACTACGT 2027 Qy 1768 CTTCACAGGCTGCTAACAGTAAACCTTTCAGGACTCTTTCTT	RESULT 14 Sequence 5. Application US/09982543A APPLICANT SIMPARION WORNGORIC PROFEIN-SPECIFIC CELL SURRACE RECEPTORS AND USES TITLE 0P INVESTION THEORY. 2014.8 FILE REFERENCE: CIPLE-04-543 CURRENT FALLACATION NOWERS: US/09/82,543A CURRENT FILING DATE: 201-10-18 FROM THE INFORMATION: THEREPORE 19/448,371 NUMBER FILING DATE: 201-10-18 FROM THE INFORMATION: 1935-66-2 SEQ 1D NOS -152 SEQ 1D NOS -152 SEQ 1D NOS -153 SERVINE: 592 TYPE: DATE OF THE PART O

	Qy 579 Db 828	Oy 639 GGAACAGGATGAAGCATTTATTCCAGTAGGAGAATCACTGAAAGACCTGATTGACCAGTC	QY 699 ACAAAGCTCTGGTAGTAGGATCTGGATTACCTTTATTGGTTCAGCGAACTATTGCCAAACA	OY 759 GATTCAGATGGTTCGGCAGGTTGGTAAGGGCCGGTATGGAGAAGTATGGATGG	QY 819 GCGTGGTGAAAAGTGGCTGTCAAAGTATTTTTACCACTGAAGAAGCTAGCT	OY 879 AGAAACAGAAATCTACCAGACGGTGTTAATGCGTCATGAAAATATACTTGGTTTTATAGC	Oy 939 TGCAGACATTAAAGGCACCGGTTCCTGGACTCAGCTGTATTTGATTACTGATTACCATGA	Qy 999 GAATGGGTCTCTGTATGACTTCCTGAAATGTGCCACCCTGGACACCAGAGCCTACTCAA	OY 1059 GITAGCITALICIGCIGCCIGIGGICGIGCCACCACACACACAAATITAIGGCACGCA D 1308 AITGGCITAITCAGCIGCGIGGGICGIGCCACCACACACACAGAAAITIAIGGCACCCCA	1119	1179	OY 1239 AGTTGACATACCCTTGAACACCGGGGGGGGCGCGGGGGGGG	QY 1299 GGACGAGAGCCTGAGTAAAAACCATTCCAGCCCTACATCATGGCTGACATCTACAGCTT	Qy 1359 TGGTTGATCATTTGGGAGATGGCCCGTCGCTGTATTACAGGAGAATCGTGGAGGAATA	OY 1419 TCAATTACCATATTACAACATGGTGCCTAGTGACCCATCTTATGAAGACATGCGTGAGGT 	Qy 1479 CGTGTGTGAAACGCTTGCGGCCAATCGTCTTAACCGCTGGAACAGTGATGAATGTCT DIT 1728 TGTGTGTGTGTAAACGTTTGCGGCCAATTGTGTCTAATCGGTGGAACAGTGATGTGTTTTGTGTGTTGTGTGTG
1539 TCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCATAATCCAGCATCCAGACTCAC		4 0	1768 CTTCACAGGCTGCTAACAGTAAACCTTTCAGGACTCT 1804 	T 15 -286-152A-37 uence 37. Application US/10286152A	lication No. 1820030134308A1 ERAL INFORMATION: Alcon Research, Ltd.	AFFLICAN: CLAIK, ADDOCT, ADDOCT, ADDOCT, TITLE OF INVENTION: BOTH MORPHOLD PROPERTY OF THILE OF INVENTION: and Their Use in the Diagnosis and Treatment of Glaucoma FILLE DE REFREISNCE: 2112 US	CURRENT FILING DATE: 202-02-28 NUMBER OF SEQ ID NOS: 54 SOFTWARE: Patentin version 3.1	; SECTIFIC 2932 ; TYPE: DNA ; ORGANISM: homo sapiens	Cuery Match Query Match As 8, Score 1387, DB 6; Length 2932; Best Local Similarity 87.8%; Pred. No. 0; Matches 1561: Conservative 0: Mismatches 205; Indels 11: Gans 4:	GCGAATTGGACAATGACTATACATTACATTACATTGGGAGC 98 TACAATTGAACAATGACTCAGCTATACATTACATTGGGAGC 34			GGCACCTTACCTTTCTTAAAATGCTATTGCTCAGGACACTGCCCAGATGACGCTATAA 	OGRIGACITOS CONTINUES DE CONTROL CONTROL CONTROL CONTROL DE CONTRO	AACCACATTAACTTCTGGGTGTATGAGTATGAGGGCTCTGATTTTCAATGCAAGGATTC	ACCAAAAGCCCAGCTACGCAGGACAATAGAATGTTGTGGACCAATTTGTGCAACAATA

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Search completed: December 9, 2005, 19:34:45 Job time : 1042 secs

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55434, A 205, App 54, App 209, App 40032, A 52435, A 44445, A 58043, A

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Searched:

Database

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1148 TGAGACAGTGGCAGTCAAGATCTTTCCCTATGAGGAGTATGCCTCTTGGAAGACAGAGAA 1207
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Squence 7. Application US/10420192

Publication No. US2005026057941

SGRUERAL INFORMATION:

APPLICANT: Lin, Herbert Y.

APPLICANT: Weinberty, Robert A.

APPLICANT: Weinberty, Robert A.

TITLE OF INVENTION: TGF-Ber Type Receptor CDNAs Encoded Products and Uses TITLE OF INVENTION: Therefor TITLE OF INVENTION: Therefor TITLE OF INVENTION: Therefor TITLE OF INVENTION THRERS: US/10/420,192

CURRENT APPLICATION NUMBER: US 09/584,929

PRIOR APPLICATION NUMBER: US 09/584,929

PRIOR PLING DATE: 1099-06-01

PRIOR PLING DATE: 1999-06-23

PRIOR PLING DATE: 1999-06-23

PRIOR PLING DATE: 1999-09-23

PRIOR PLING DATE: 1999-09-23

PRIOR PLING DATE: 1999-10-31

NUMBER OF SEQ ID NOS: 8

SOFTHARB: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      885 AGAAATCTACCAGACGGTGTTAATGCGTCATGAAAATATACTTGGTTTTATAGCTGCAGA
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ALIGNMENTS
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LOCATION: (336)...(2038)
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ORGANISM: genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2090
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    US-10-420-192-7
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Sequence 35470, A
Sequence 39254, A
Sequence 32, Appl
Sequence 208, App
Sequence 201, App
Sequence 201, App
Sequence 211, App
Sequence 206, App
Sequence 206, App
Sequence 37, Appl
Sequence 35, Appl
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11, Appl
64192, A
                                                                                                                                  December 9, 2005, 17:16:24 ; Search time 167 Seconds (without alignments) 4058.673 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                             1813
1 CTAGTGGATCCCCCGGGCTG......TTCAGGACTCTGCAGAATGC 1813
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Sequence 1
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 US-10-420-192-7
6 US-10-750-185-35470
6 US-10-750-185-33450
7 US-11-117-187-211
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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1005 GTCTCTCTATGACTTCCTGAAATGTGCCACCCTGGACACCAGAGCCCTACTCAAGTTAGC 1064
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Publication No. US20050260603A1
GENERAL INPORMATION:
APPLICANT: MAI GENOUICS, INC.
APPLICANT: ERRR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: BENER, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
FILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFREENCE: MAIL100-2
CURRENT FALING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
SOFTWARE PELLING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
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Best Local Similarity 56.1
Matches 105; Conservative
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US-10-750-185-35470/c
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US-10-750-185-35470
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LENGTH: 2197
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APPLICANT: DATE GENORICS, INC.
APPLICANT: DATE GENORICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: PANTIN, Dennis
APPLICANT: FANTIN, Dennis
APPLICANT: FANTIN, Dennis
APPLICANT: FANTIN, COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILER REFERENCE: MAILOD-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
SOFTWARE PELENCE: SUE-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENT VERSION 3.1
SEQ ID NO 39254
LENGTH: 1481
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Pred. No. 0.00023;
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, SUE K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFREENCE: MMILLOD-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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; Sequence 53450, Application US/10750185
; Publication No. US20050260603A1
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Best Local Similarity 65.09
Matches 67; Conservative
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SEQ ID NO 211
LENGTH: 1082144
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LENGTH: 94905
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2.1%; Score 38; DB 6; Length 840
Best Local Similarity 53.3%; Pred. No. 0.044;
Matches 80; Conservative 0; Mismatches 70; Indels
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APPLICANT: Davis, Lisa M.
TITLE OF INVENTATION: Breast Cancer Biomarkers
FILE PERENEW: 04-164-US
CURRENT APPLICATION: Breast Cancer Biomarkers
FILE PEPERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-130
PRIOR PLICATION NUMBER: US 60/631,702
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR PILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-07
NUMBER OF FOO ID NOS: 511
SOFTWARE: Patentin version 3.3
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PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 53450
LENGTH: 840
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; Publication No. US20050260659A1
; GENERAL INFORMATION:
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; ORGANISM: Bovine 19866880986810
US-10-750-185-53450
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Best Local Similarity 54.0°
Matches 75; Conservative
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ORGANISM: Homo sapiens
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US-11-117-187-208

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1071603 GAGTAGATGTCATTTATATAGATTTGAGTATAGAACTAGAACCGCAACCAATTCCCAAAAG 1071544
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Publication No. US20050266560A1

GENERAL INFORMATION:
APPLICANT: PREUS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT AFTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REPERBNCE: ARCD:309US
CURRENT FILING DAFE: 2005-04-28
FRIOR APPLICATION NUMBER: US/11/117, 187
FRIOR APPLICATION NUMBER: 60/125, 219
FRIOR PILING DATE: 1999-03-17
FRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patent In Ver. 2.1
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APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILLE REPERENCE: ARCD:309US
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/11/117,187
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PALENTIN Ver: 2.1
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Pred. No. 21;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-208
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Best Local Similarity 57.4%;
Matches 85; Conservative
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Best Local Similarity 57.4%;
Matches 85; Conservative
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RESULT 10
US-11-117-187-211
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                                                                                                                                                                                                                  APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:30.904
CURRENT APPLICATION NUMBER: US/11/11/187
CURRENT APPLICATION NUMBER: US/09/531,120
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR PLLING DATE: 2000-03-17
PRIOR PRIOR PLING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 207
LENGTH: 82596
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Publication No. US2005056560A1

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

COPENHAVER, GREGORY

TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS

FILE REPERENCE: ARCD:309US

CURRENT APPLICATION NUMBER: US/11/117,187

CURRENT FILING DATE: 2005-04-28

PRIOR FILING DATE: 2000-01-7

PRIOR FILING DATE: 1999-03-18

NUMBER OF SEQ ID NOS: 212

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 208

LENGTH: 94905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0%; Score 35.6; DB 7; Length 82596; Best Local Similarity 57.6%; Pred. No. 6.7; Matches 83; Conservative 0; Mismatches 59; Indels 2;
                                          1071543 CTAAAGTAGTATTTCCTTGTTAGAAGAT 1071516
1706 GAAGGGTGGAGTTAGCATGGACTAGGAT 1733
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                                                                                                                                                      Sequence 207, Application US/11117187; Publication No. US20050266560A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-207
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US-11-117-187-207/c
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1590 CAGACTCACAGCTTTGAGAATCAAGAAGACGCTCGCAAAGATGGTTGAATCCCAGGATGT 1649

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988011 CTAGATGTCATGTGGATGATTGAGTATAAGAACTAAAACCGCAACTGGTTCCCAAGGGCT 988070
91513 CACCATCAAAGCTTTGAGAAGCAATAAGAAGCTATGTCAGCTTTTTGGAGTCAAAAATATGA 91454
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Publication No. US20050266560A1

GENERAL INFORMATION:
APPLICANT: PRRUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD: 3090'S
CURRENT PILING DATE: 2005-04-28
FRICR APPLICATION NUMBER: US/9/531,120
FRICR APPLICATION NUMBER: 60,125,219
FRICR FILING DATE: 1999-03-17
FRICR FILING DATE: 1999-03-18
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                                                                                                  1650 AAAGATTTGACAAACAGTTTTGAG--AAAGAATTTAGACTGCAAGAAATTCACCCGAGGA 1707
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APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FAVIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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2.0%; Score 35.6; Di
Best Local Similarity 57.6%; Pred. No. 38;
Matches 83; Conservative 0; Mismatches
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MHI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana US-11-117-187-211
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SEQ ID NO 29585
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APPLICATION NUMBER: US/09/531,120
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| Publication No. US2005026650A1
| Publication No. US2005026650A1
| GENERAL INFORMATION:
| APPLICANT: PREUS, DAPHNE
| APPLICANT: COPENHAVER, GREGORY
| TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
| FILE REFERENCE: ARCD:309US
| CURRENT APPLICATION NUMBER: US/11/117,187
| CURRENT APPLICATION NUMBER: US/09/531,120
| PRIOR PELICATION NUMBER: US/09/531,130
| PRIOR PELICATION UMBER: US/09/531,130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 206, Application US/11117187
Publication No. US20050266560A1
GENERAL INPORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:30908E: US/11/117,187
CURRENT APPLICATION NUMBER: US/11/117,187
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                                                                                                                                         DB 6; Length 1342;
                                                                                                                                                                                              93; Indels
                                                                                                                                       Score 35.2; DB
Pred. No. 0.51;
0; Mismatches
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                                                                                                                                    Query Match
Best Local Similarity 49.5%;
Matches 91; Conservative
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                    TYPE: DNA
CRGANISM: Bovine
US-10-750-185-29585
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11-117-187-184/c
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LENGTH: 1342
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59912 TTCACCATCAAAGCTTTGAGAAGCAAGAAGGATTGGTTAGTGTTTTGGAGTCGAATAT 59853
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REPERENCE: 09138.6000-000000;
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR PELLING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
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Pred. No. 40;
0; Mismatches 42; Indels
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1.9%; Score 34.8; D
Best Local Similarity 56.8%; Pred. No. 11;
Matches 84; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: CV. PRIOR FILING DATE: 2000-03-17
PRIOR PEDLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.1
SEC ID NO 206
LENGTH: 72600
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Publication No. US2050260603A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, TOM
                                                                                                                                                                                                                                           ; ORGANISM: Arabidopsis thaliana US-11-117-187-206
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Best Local Similarity 58.44
Matches 59; Conservative
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US-10-750-185-57651/c
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APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILLOG-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 1843
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1.9%; Score 33.6; DB 6; Length 1843;
Best Local Similarity 48.4%; Pred. No. 2.2;
Matches 93; Conservative 0; Mismatches 99; Indels 0.
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; ORGANISM: Bovine 19866880756367
US-10-750-185-57651
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/gene="BMPR1A"
/locus_tag="HCM4130"
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AY411156 HOMO SADI
AY411157 PAN LYOGI
BM473726 AGENCOURT
AU124197 AU124197
CV558493 UI-M-HZO-
CX204646 MUSSO7540
AK086130 MUS MUSCU
CK638737 UI-M-HOO-
AY418115 MUS MUSCU
CF744610 UI-M-GYO-
DR156725 HESCZ 69
CV557698 UI-M-HZO-
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CD351417 UI-M-GIO-
AY418114 Pan trogl
BUJ52346 AGENCOURT
CN530503 UI-M-HOO-
CO46435 UI-M-HOO-
CD525514 UI-M-GIO-
AU124052 AU124052
                                                                      December 9, 2005, 13:31:58 ; Search time 5033 Seconds (without alignments) 16853.761 Million cell updates/sec
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1813
1 CTAGTGGATCCCCCGGGCTG.....TTCAGGACTCTGCAGAATGC
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                 41078325 segs, 23393541228 residues
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Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
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AY411156
AY411157
BM473726
AU224197
CV558493
CX54646
AK086130
CK638737
AY418115
CF744610
CV57698
AY418113
CD351417
CD351417
BU152346
CN530503
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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Maximum DB
                                               OM nucleic
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					ALIGNMENTS	
RESULT 1 AY411158						
1.00.1	AVA	AV411158			ANC	1inear GSS 16-DEC-2003
DEFINITION	-	Mus musculus	ā		e, VIRTUAL TRANSCRIP	partial se
	gen	genomic su	survey se	sednence	ice.	
ACCESSION	AY4	11158	•	į		
VERSION	AY4.	11158.1	GI:39	976712	756	
SOUTHOR	2 X		מפווסל) פו		moise)	
MOTINGO) i	200000000000000000000000000000000000000				
HIS TARGET SHE		aryota;	Metazo	, E	Craniata; Verteb	Vertebrata; Euteleostomi;
	Mam	nalia; E	Sutheria		Mammalia; Eutheria; Euarchontoglires; Glires	Rodentia;
REFERENCE	ָרָ בַּי	(bases 1	ro 1521)	1	a, furidae, furinae, fur	•
AUTHORS	<u>.</u>	k A	Glano	X	S. Nielson.R. Thomas	P. Kejariwal.A.
	Tod	1, M.A.	Tanenb	m,	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F.	, Murphy, B.,
	Fer	riera, S.	, Wang,	Ü	Zheng, X.H., White, T.J.,	Sninsky, J.J
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PUBMED	146	71302	2	_		
REFERENCE	0	(bases 1 to 1521)	to 15;	(17		
AUTHORS	Claı	rk, A.G.,	Glano	vaki	Thomas	,P., Kejariwal,A.,
	Tode	1, M.A.,	Tanenb	aum,	ч., Ги,	., Murphy, B.
	Fer	riera, S.	, Wang,	ر ان	Ferriera, S., Wang, G., Zheng, X.H., White, T.J.,	Sninsky,J.J
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	them	base	on alic	an di	int.	
FEATURES		. З.	cation/	g,	lifiers	
source	ø	۲,	1521	:	•	
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11; Gaps

DB 10; Length 1521; 69; Indels

Query Match 76.6%; Score 1389.6; Best Local Similarity 94.8%; Pred. No. 0; Matches 1452; Conservative 0; Mismatches

CO045435 CD352514 AU124052

667.2 666.6 664.8 664.8 662.2

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gene, VIRTUAL TRANSCRIPT, partial sequence,
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1 (bases 1 to 1532)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                               1021 TAAAGAGCAAAAACATCCTCATCAAGAAAAATGGGAGTTGCTGCATTGCTGACTGGGCC
                                                                                  GCTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATGGTGCCTA
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                 TGAAGAGCAAAAACATCCTTATTAAGAAAAATGGTAGTTGCTGTATTGCTGACCTGGGCCC
                                                                    TAGCTGTTAAATTCAACAGTGACACAAATGAAGTTGACATACCCTTGAACACCCAGGGTGG
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on allgament.
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Pan troglodytes
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VERSION
KEYWORDS
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/mol_type="genomic DNA'
/db_xref="taxon:9598"
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/gene="BMPR1A"
/locus_tag="HCM4130"
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AU124197 874 bp mRNA linear EST 01-AUG-2002 AU124197 NT2RM2 Homo sapiens cDNA clone NT2RM2001814 5', mRNA sequence.
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/cell_line="NT2"
/colo= lib="NT2RM2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
Unpuli,Y.- (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 874)

Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix:
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                           841 TCTCTATGAACTTCCTGAAATGTGCTACACTGGACACCAGAGCCCTGCTTAAATTGGCTT
                                                                                                           901 ATCCAGCTGGCCTGGGGCCTGGGCCACCTGCCCCCAGAAATTTATGGGCCCCCCAAGAAAA
                                                                                                                                                         1125 -GCCTGCAATTGCTCAT-CGAGACCTGAAGAGCAAAAACATCCTTATTAAGAAAA 1178
                                                                                                                                                                            ATTCTGCT-GCCTGTGGTCTGTGCCACCTCCACACAAATTTATGGCACGCAAGGCAA-
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90.1%; Pred. No. 6.6e-209;
live 0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812,
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM2001814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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AU124197.1 GI:10948913
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Mammalia; Eutheria;
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Matches 787;
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5562094"
/tissue_type="duodenal adenocarcinoma, cell line"
/tab_host="bulloB (phage-resistant)"
/clone_lib="NHH MGC 88"
/note="Organ: small_intestine, Vector: pCMV-SPORT6,
Site_l: Not!, Site_2: Sall; Cloned unidirectionally,
oligo_dT primed. Ayerage insert size l.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NHH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CATAACTAATGGCCATTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAAACCACGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGCTACGCAGGACAATAGAATGTTGTCGGACCAATTTGTGCAACCAATATTTGCAGCC
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                                                                                                                                                                                                                                       Length 1121;
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                                                                                                                                                                                                                                     Score 774.6; DB 3;
Pred. No. 1.8e-220;
0; Mismatches 120;
                                                                                                                                                                                                                                     42.7%;
ilarity 87.7%;
Conservative 0
                                                                                                                                                                                                                                                        Similarity
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Matches 891;
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/db_xref="Laxon:10090"
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/dev stage="newborn 1,5,15 and embryos 15,16,17,18 dpc"
/db_host="DH10B (T1 phage resistant)"
/clone=11b="NHLB MAD_HT20"
/note="Organ: EPs' Vector: PXX-Asc; Site 1: EcoR 1;
Site 2: Not 1; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor digested with Not1 and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH)."
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousef1.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AAATGGATCTCTCTATGACTTCCTGAAATGTGCCACACTAGACACCAGAGCCCTACTCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTAGTTGCTGTATTGCTGACCTGGGCCTAGCTGTTAAATTCAACAGTGACACAAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TGGAAGTTGCTGTATTGCTGACCTGGGCCTAGCTGTTAAATTCAACAGTGATACAAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.5%; Score 734; DB 7; Llarity 92.5%; Pred. No. 2.7e-208; Conservative 0; Mismatches 56;
                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
                                                                                         Seq primer: pXX-5.
Location/Qualifiers
                                                                                                                               .915
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Matches 817;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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   CACTGCCCCCTGTTGTCATAGGTCCGTTTTTTGATGGCAGCATTCGATGGCTGGTTTTGC 180
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                                                         181 TCATTTCTATGGCTGTCTGCATAATTGCTATGATCATCTTCTCCAGCTGCTTTTGTTACA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 915)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CV558493.1 GI:54445126
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360 748 420 808 480 868 540 928 600

508 180 568 240 628 300

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Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930007102 product:bone morphogenetic protein AK086120. type 1B, full insert sequence.
AK086130.1 G1:26351960
HTC; CAP transor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTACCATGAGAATGGGTCTCTATGACTTCCTGAAATGTGCCACCCTGGACACCAGAG 1048
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia;
                                                               61 GCAAGGATTCACCGAAAGCCCAGCTACGCAGGACAATAGAATGTTGTCGGACCAATTTGT
                                                                                                                         541 GCTGGTTTAGAGAAAAAAATCTACCAGACGGTGTTAATGCGTCATGAAAATATAGTTG
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GCAACCAATATTIGCAGCCTACACTGCCCCCTGTCGTTATAGGCCCATTCTTTGATGGCA
                                                                                                                                                                                     241 TCTCCAGCTGCTTTTGCTATAAAGCATTATTGTAAGAGTATCTCAAGCAGGGGTCGTTACA
                                                                                                                                                                                                                                                                                             ACCGTGACTTGGAACAGGATGAAGCATTTATTCCAGTAGGAGAATCACTGAAAGACCTGA
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Mus musculus (house mouse)
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S Williams, C., Wirta, V., Lundeberg, J. and Frisen, J.

Expressed sequence tags of cDNA clones from murine neurospheres
L Unpublished (2005)
Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
AlbaNova University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel: 44685378313.
Fax: 44685378318.
Fax: 44685518481
Email: cecilia williams@biotech.kth.se
Seq primer: MIRREW.
                                                                                                                                                                                  AC----AAACAGTTTTGAGAAAGAATTTAGACTGCAAGAAATTC----ACCCGAGGAAGG 1710
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/cell type="Early passage neurosphere"
/dev_stage="Adult"
/clone_lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVSport6.0; A cDNA
library was constructed in pCMVSport6.0 from RNA isolated
from neurospheres of adult male and female mice. Custom
normalized cDNA library by Invitrogen/ResGen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                 CX204646 MNSO7540 MOUSE Neurosphere Normalized cDNA library Mus musculus cDNA 5', mRNA sequence.
                 TGTGTGTGTGAAACGCTTGCGGCCAATCGTGTCTAACCGCTGGAACAGCGATGAATGTCT
                                                                            TCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCCATAATCCAGCATCCAGACTCAC
                                                                                                                       AGCITTGAGAATCAAGAAGACGCTCGCAAAGATGGTTGAATCCCAGGATGTAAAGATTTG
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BST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euti
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
/mol_type="mRNA"
/strain="c57BL/6"
/db_xref="taxon:10090"
/sex="MALE"
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/note="unnamed protein product; bone morphogenetic protein receptor, type 1B (MGD|MGI:107191, GB|NM_007560, evidence: BLASTN, 100%, match=1775)
                                                                                                                                                                                                                                                                               /translation="MLLRSSGKLNVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVN
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                                                                                                                                                                                                                                                                                                                                                      IGLEQDETYIPPGESIRDLIEQGSSGSGSGLPLLVQRTIAKQIQMYKQIGKGRYGEV
WMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLY
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155. 1663
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                                                                                                                                                                                                        /codon_start=1
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

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7 Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-reseggc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
                                            Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636
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/db_xref="taxon:I0090"
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/ Branta-Cyler Head"
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/ dev stage="Upper Head"
/ dev stage="S-10.5 dpc"
/ lab_host="DHIOB (TI phage resistant)"
/ lote="Organ: Head; Vector: pXX-Asc; Site 1: EcoR I;
/ lote="Organ: Head; Vector: pXX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcos
gel.First strand cDNA synthesis was primed with Oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not! and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGATGATCAGGGAGAAACCACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGAT 381
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  National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.5%; Score 715.6; DB 7; Best Local Similarity 94.9%; Pred. No. 8.5e-203; Matches 739; Conservative 0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6"
                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                Seq primer: pYX-5.
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires; Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 779)
NIH-MGC http://mgc.nci.nih.gov/.
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742

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REFERENCE AUTHORS

qg		ò	247 TGCTCAGGACACTGCCCAGATGACGCTATTAATAA
8 %	802 GTATGGATGGGTAAATGGCGTGGTGGAAAAGTGGCTGTCAAAGTATTTTTACCACTGAA 861 	q ò	100 TGCCACCACCACTGTCCGGAAGACTCAGTCAACAA 307 TTTGCCATTATAGAAGAAGATGATGAGGGAGAAAA
ç, Db	862 GAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACGGTGTTAATGCGTCATGAAAAT 921 	· a ò	
ò :	AIACTTGGTTTTATAGCTGCAACATTAAAGGCACCGGTTCCTGGACTCAGCTGTATTG	qa ;	
3 8	ATTACTGATTACCATGAGGGGGGGGGGGGGGGGGGGGGG	à a	280 GAATGCTGCACAGAAGGAATGAGTGTAATAAAGA
qa	661 ATTACTGATTACCATGAAAATGGATCTCTCTATGACTTCCTGAAATGTGCCACACTAGAC 720	ò	484 GTTATAGGCCCATTCTTTGATGGCAGCGTCCGATC
ò d	1042 ACCAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCCTGTGGTCTGTGCCACCTCCACC 1100	අ	340 AAGGACAGAGATTTTGTTGATGGCCCCATACACC
- H 11000		qa	
AY418115 LOCUS		λö	604 AGTATCTCAAGCAGAGGTCGTTACAACCGTGACTT
DEFINITION	NN Mus musculus BMPR1B gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	qa ,	
ACCESSION VERSION KEYWORDS		y dg	664 GTAGGAGATCATTGAGAGGCTGATTGACCAGTT 514 CCTGGAGAGTCCCTGAGAGACTTGATCGAGGGTTC
SOURCE ORGANISM		'n	
	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciuroanathi, Muroidea, Muridae, Murinae, Mus	QD	574 CTCCCTCTGCTGGTCCAAAGGACAATAGCTAAGCA
REFERENCE AUTHORS		'n	
	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Fertiers, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,	q :	634 AAAGGCCGCTATGGCGAGGTGTGGATGGGAAAGTC
TITLE		중 名	694 GTGTTCTTCACCAGGAAGAAGCCAGCTGGTTAC
JOURNAL PUBMED		λo	904 TTAATGCGTCATGAAAATATACTTGGTTTTATAGC
AUTHORS		qa	754 CTGATGCGCATGAGAATATTCTGGGGTTCATTG
	Journal Americans, Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Carqill, M.	ò	964 IGGACTCAGCIGTATTIGATTACTGATTACCATGA
TITLE JOURNAL		qq	
COMMENT	KOCKVILIE, MD 20890, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.	ò 8	1024 AAATGTGCCACCTGGACACAGAGCCTACTCAC
FEATURES sourc	ω.	ìò	
	/organism="Mus musculus" /mol type="genomic DNA" /Ab	qq	
gene		δλ	1144 GACCTGAAGAGCAAAAACATCCTTATTAAGAAAAA
ORIGIN	/locus_tag="HCM6449"	Ωρ	994 GACTTGAAAAGTAAAAACATCCTGGTGAAGAAAA
Query Match Best Local	39.2%; Score 710; DB 10; Length 1509; Similarity 68.6%; Pred, No. 5.2e-201; Todal 0.	oy G	1204 GGCCTAGCTGTTAAATTCAACAGTGACACAAATGA
2	vactive of minomicaline 1957 finders 5; dafo	ò	1264 GTGGGCACCAGGCGGTACATGGCTCCAGAAGTGCT
S & ,	99	qq	1114 GTTGGCACCAAGCGCTATATGCCTCCAGAAGTGC

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CAAGGCAAGCCTGCAATTGCTCATCGA 1143
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                            ACCACGTTAACTTCTGGGTGTATGAAG 366
                                                                                           TATTIGCAGCCTACACTGCCCCCTGTC 483
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TGGCGTGGAGAAAAGGTGGCTGTGAAA 693
                                                                                                                                                                                                                                                                                                               AGAGAAACAGAAATCTACCAGACGGTG 903
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                                                           CCAAAAGCCCAGCTACGCAGGACAATA 426
                                                                          ccarrctarcaadadarcaar 279
                                                                                                                                                       recircierracaaacarracreraag 603
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sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University lowa Brain Anatony Project (BNAAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."	Query Match Best Local Similarity 95.2%; Score 707.6; DB 6; Length 783; Best Local Similarity 95.2%; Pred. No. 2.1e-200; Matches 739; Conservative 0; Mismatches 36; Indels 1; Gaps 1; Ov 318 AGAAGAAGATGATC-AGGGAGAAACCACGTTAACTTCTGGGTGTATGAAGTATGAAGGTT. 376	1 AGAAGAAGATGAAGGGAGAAACCACATTAACTTCTGGGTGTATGAAGTATGAAGGCT 6	Qy 377 CTGATTTTCAATGCAAGGATTCACCAAAAGCCCAGCTACGCAGACAATAGAATGTTGTC 436	Oy 437 GGACCAATTTGTGCAACCAATATTTGCAGCCTGCCCCTGTCGTTGTTATAGGCCCAT 496	Qy 497 TCTTTGATGGCAGCGTCCGATGGCTGTGTTCTTATGGCTGTTGTTGTCG 556	OY 557 CCATGATCGTCTTCTCCAGCTGCTTCTGTACAAACATTACTGTAACAGTATCTCAAGCA. 616	Qy 617 GAGGICGITACAACCGIGACTIGGAACAAGGAITAITAITCCAGIAGGAGAAICAC 676 	Qy 677 TGAAAGACCTGATTGACCAGTCACAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTGG 736	OY 737 TTCAGGGAACTATTGCCAAACAGATTCAGATGGTTCGGCAGGTTGGTAAGGGCCGGTATG 796	OY 797 GAGAAGTATGGGTAAATGGCGTGGAAAAAGTGGCTGTCAAAGTATTTTTACCA 856	QY 857 CTGAAGAAGCTAGCTCGTTTAGAGAAACAGAAATCTACCAGACGTCTTAATGCGTCATG 916	Oy 917 AAAATATACTTGGTTTTATAGCTGCAGACATTAAAGGCACCGGTTCCTGGACTCGGCTGT 976	QY 977 ATTTGATTACTGATTACCATGAGAATGGGTCTCTCTATGACTTCCTGAAATGTGCCACCC 1036	OY 1037 TGGACACCAGAGCCCTACTCAGTTAGCTTATTCTGCTGCTGTGGTCTGTGCCAC 1092 	RESULT 12 DR156725 LOCUS LOCUS DEFINITION HESC2_69 D09.G1 A035 NIH MGC_258 Homo sapiens cDNA clone IMAGE:7965451 57, mRNA sequence. ACCESSION DR156725 VERSION DR156725.1 G1:67868885 KEYWORDS EST.
Qy 1324 TTCCAGCCCTACATGGTGACATCTACAGCTTTGGTTTGATCATTTGGGAGATGGCC 1383 Db 1174 TTCCAGTCCTACATTATGGCTGACATGTACAGCTTTTGGACTCATCTTGGGAGGATTGCA 1233 Qy 1384 GGTCGCTGTATTACAGGAGGAATCGTGGAGGAGATATCAATTACCATATTACAACATGGTG 1443 Db 1234 AGGAGATTTCTGGAGGATATAGTGGAAGAATACCAGCTTCCCTATCACGACCTGGTG 1293	Qy 1444 CCTAGTGACCATCTTATGAAGACATGCGTGAGGTCGTGTGTGAAACGCTTGCGGCCA 1503 Db 1294 CCCAGTGACCCTTCTTATGAGGACATGAGAATTGTGCATGAAGATTACGGCCT 1353 Ov 1504 ATCGTCTCTAACCGCTGGAACAGTGATGAATGTCTTCGAGCCGTTTTGAAGCTGATGTC 1563	1354 TCATTCCCCAATCGATGGAGCAGTGATGTGTCTCAGGCAGATGGGGAAGCTTATGACA	Qy 1564 GAATGCTGGGCCCATAATCCAGACTCACAGACTTTGAGAATCAAGAAGACGCTC 1623 Db 1414 GAGTGCTGGGCGCAGAATCCTGCCTCCAGGCTGACGCCCTGAGAGTTAAGAAAACCCTT 1473	Qy 1624 GCAAAGATGGTTGAATCCCAGGATGTAAAGATTTGA 1659	RESULT 11 CF744610 1.OCHS CF744610 783 hx mbMA linesy per 10_000-2003	ITION UI-M-GYO-clt-d-20-0-UI.1 NIH BMAP_GVO Mus musculus cDNA clone IMAGE:30617467 5', mRNA sequence. SION CF744610	S EST. Mus musculus (house mouse) ISM Mus musculus	Everaryous, metazoa, choracas, Cransaca; verebraca; buceroscomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Murcidae; Murinae; Mus. REFERENCE 1 (bases 1 to 783)		Tissue Procurement: Dr. James Lin, University of Iowa Tissue Procurement: Dr. James Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa	Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html This clone was contributed by the Brain Molecular Anatomy Project	Seq primer: pYX-5. FEATURES Location/Qualifiers 1783	/organism="minum" //organism="minum" //ortain="CS7BL/6" //db_xref="minum" //db_xref="minum" //db_xref="minum"	/clone=lnades:301/46/" /tissue_type="whole brain" /dev_stage="1,5, and 15 days newborn" /lab_host=="HilloB (TI phage resistant)" //ab_host=="hilloB (TI phage resistant)"	/orde=Torgan: Brain; Vector: pYX- Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarcse gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag

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CV557698 763 bp mRNA linear EST 22-OCT-2004 UI-M-HZO-ctc-n-16-0-UI.rl NIH_BMAP_HZO Mus musculus cDNA clone IMAGE:30695271 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952 GGCACCGGTTCCTGGACTCAGCTGTATTTGATTACTGATTACCATGAGAATGGGTCTCTC 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGACTTCCTGAAATGTGCCACCCTGGACACCAGAGCCCTACTCAAGTTAGCTTATTCT 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 GGTACAGGTTCCTGGACTCAGCTCTATTTGATTACTGATTACCATGAAATGGATCTCTC 600
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html
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                                                                                                                                                                                                                           AGTGGGTCTGGACTACCTTTATTGGTTCAGCGAACTATTGCCAAACAGATTCAGATGGTC 360
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATGACTTCCTGAAATGTGCTACACTGGACACCAGAGCCCTGCTTAAATTGGCTTATTCA
<u> AGTGGATCTGGATTACCTTTATTGGTTCAGCGAACTATTGCCAAACAGATTCAGATGGTT</u>
                                                                                                                                                                                                                                                                                                                                                                            TACCAGACGGTGTTAATGCGTCATGAAAATATACTTGGTTTTTATAGCTGCAGACATTAAA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mus musculus
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KEYWORDS
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/cell type="human embryonic stem cells"
/cell line="BGOI"
/lab_Eost="DHIOB-T1 phage-resistant E. coli"
/clone lib="HIM MGC 258"
/clone lib="HIM MGC 258"
/note="Vector: pExpress-1; Site 1: Not1; Site 2: EcoRV;
/Not cell mass of blastocyst stage embryos and differentiated to an early endodermal cell type. Cell line id and NIH Registry designation is BGOI. Positive for GATA4, MixL1, Msx1, HNF4alpha expression; negative for AFP expression. Passage number 40. cDNA primed using oligo-dT primer: 5'-pGACTAGTCTAGANCGCGAGCGCCCC(7)25-3' and cloned into the EcoRV/Not1 sites of pExpress-1. This primary library is non-normalized (normalized primary library is non-normalized (normalized by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Note: this is a Mammalian Gene Collection library."
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                                                                                                                                                                                                              Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: BresaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.ev.g column: 17
Plate: LLAM 17072 row: g column: 17
Seq primer: JENREV (CAGGAAACAGCTATGACC)
High quality sequence stop: 826.
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                                                  Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIGCCCCCTGTTGTCATAGGTCCGTTTTTTGATGGCAGCATTCGATGGCTGGTTTTGCTC
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                                                                                                Hominidae, Homo.
1 (bases 1 to 826)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 1.3e-199;
0; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7965451"
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  sapiens (human)
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Matches 750; Conserv
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1509 bp DNA linear GSS 17-DEC-2003
Homo sapiens BMPR1B gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
                      TTCGAGCCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCATAATCCAGCATCCAGACTCA 1597
                                            661 TTCGAGCAGTTTTGAAGCTAATGTCAGAATGTTGGGCCCCATAATCCAGCCTCCAGACTCA 720
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1 (bases 1 to 1509)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferricar, S., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferricar, S., Wang, G., Eng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGCCATTATAGAAGAAGATGATCAGGGAGAAACCACGTTAACTTCTGGGTGTATGAAG 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark, A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Glark,A.G., Glanowski,S., Nielson,R., Lu,F., Murphy,B., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Snockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 AAGAAAGAGGATGGTGAGAGTACAGCCCCCCCCCCCCCGTCAAAGGTCTTGCGTTGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCCGGAAAATGGAGTGACGTTAGCACCAGAGGACACCTTACCTTTAAAATGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 INTGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAAGCCCAGCTACGCAGGACAATA
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                                                                                                           CAGCTTTGAGAATCAAGAAGACGCTCGCAAAGATGGTTGAATC
                                                                                                                                 Score 702; DB 10;
Pred. No. 1.3e-198;
0; Mismatches 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_rref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="HCM6449"
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                                                                                                                                                                                                                                                                                                                                          AY418113.1 GI:39774073
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llarity 68.2%;
Conservative
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Homo sapiens
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Best Local Simil
Matches 1007;
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REFERENCE
AUTHORS
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JOURNAL
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AY418113
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                                                                       /db xref="taxon:10090"
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/tissue_type="whole eye"
/dev_stage="newborn 1,5,15 and embryos 15,16,17,18 dpc"
/dab_host="HUHUB (TI phage resistant)"
/clone_lib="NIH_BNAP_HZO"
/clone_lib="NIH_BNAP_HZO"
/note="Organ: By9, Vector: pXx.hac; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand CDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand CDNA was
size selected according to mRNA size fraction, ligated
with ECOR I adaptor, digested with NotI and then cloned
directionally into pYx.Aso vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 703.8; DB 7;
Pred. No. 2.9e-199;
0; Mismatches 37;
                      organism="Mus musculus"
                                          mol_type="mRNA"
strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.2%;
Matches 726; Conservative C
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/tissue type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab.host="Union Ti phage resistant)"
/clone lib="MINH BMAP GIO"
/clone lib="MINH BMAP GIO"
/clone lib="MINH BMAP GIO"
/clone lib="Organ: Brain" Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site . Doubbe strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
lowa Erain Anatomy Project (BMAP): 'Gene Discovery in the
                                                                                                                                                                                                                                                                                                                      CU351417

T69 bp mRNA linear EST 09-JUL-2003
UI-M-GIO-cgk-c-22-0-UI.rl NIH_BMAP_GIO Mus musculus cDNA clone
IMAGE:6856367 5', mRNA sequence.
     1354 TCATTCCCAAACCGGTGGAGCAGTGATGAGTGTCTAAGGCAGATGGGAAAACTCATGACA 1413
                                                                                                      1414 GAATGCTGGGCTCACAATCCTGCATCAAGGCTGACAGCCCTGCGGGTTAAGAAACACTT 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nib.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefi.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                       GAATGCTGGGCCCATAATCCAGCATCCAGACTCACAGCTTTGAGAATCAAGAAGACGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 GGACACGTGCGAATTGGACAATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NHH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Euarchontoglires, Glires, Rodentia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi, Muroidea, Muridae, Murinae, Mus
1 (bases 1 to 769)
                                                                                                                                                           GCAAAGATGGTTGAATCCCAGGATGTAAAGATTTGA 1659
                                                                                                                                                                                     GCCAAAATGTCAGAGTCCCAGGACATTAAACTCTGA 1509

    769
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="C57BL/6"

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/clone="IMAGE:6856367"
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Location/Qualifiers
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Truncated bone morphogenic protein (BMP) receptors and serine/threonine kinase receptors may be used in compositions to inhibit the effects of BMP·s such as BMP-2 and BMP-4. The truncated receptors pref. comprise the ligand binding domain, but not the serine/threonine kinase and transmembrane domains. The truncated proteins are soluble and will be excreted into supernatant by recombinant mammalian cells expressing them. Such cells can be delivered in a medium or matrix which partially impedes their mobility, thereby localising the cells to a site of bone or cartilage injury. (Updated on 25-MAR-2003 to correct PN field.)
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Copyright (c) 1993 - 2005 Compugen Ltd.
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound useful in treating cativity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating cativity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating compulates its activity is useful for preparing a medicament for treating colypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating catherapy). The sequence presented is a rat protein (shown in Table 2 of the rerapy). The sequence presented is a rat protein (shown in Table 2 of the sequence data for this patent did not form part of the printed or this patent did not form part of the printed for greening decreases.)
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                                        New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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                                                                   MTQLYTYIRLLGACLFIISHVQGQNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLK
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   Length 532;
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100.0%; Score 2838; DB 7;
100.0%; Pred. No. 8.6e-279;
ive 0; Mismatches 0;
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 Query Match 100.
Best Local Similarity 100.
Matches 532; Conservative
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N-PSDB; ADW28817.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a gent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity of one or more of the specification, a method for identifying a compound or small molecule that regulates the activity of one or more of the specification, a method for identifying a compound useful in treating complaints of or identifying a compound useful in the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating complaints its activity is useful for preparing a medicament for treating complaints its activity is useful for preparing a medicament for treating complaints its activity is useful for preparing a medicament for treating complaints (c.g. spin led. 9. spinal segmental nerve injury (CNI) in an animal (e.g. gene the respectification) which is differentially expressed during pain. Note: the specification) but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequence of the peripressed of provides or the sequence of the specification, but we obtained in electronic form directly from wIPO at
                                                                                                                                                                                                                                                          Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                   Costigan M;
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                                                                                                                    ADE61815 standard; protein; 532
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                      (first entry)
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(FARB ) BAYER AG.
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GENBANK; AAB33865.
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                                                                                                                                       This invention relates to a novel antibody or antigen-binding fragment that binds specifically to a sclerostin (50ST) polypeptide and impairs formation of a sclerostin homodimer. Specifically, it refers to an antibody that competitively inhibits binding of the sclerostin polypeptide to a bone morphogenic protein (BMP) Type I receptor binding site. The present invention describes a hybridoma cell capable of producing the antibody and a host encoding a transforming growth factor-beta (TGF-beta) binding protein known as SOST and also BEER) and methods for detection thereof Accordingly, such antibodies and osteopathic compositions of the
New antibody or antigen-binding fragment that binds specifically to sclerostin polypeptide and which inhibits binding of sclerostin polypeptide to a bone morphogenic protein, useful for increasing bone mineral content or density.
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Pred. No. 8.6e-279;
; Mismatches 0;
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ADW28802 standard; protein; 532

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such, these compositions improve bone mineralization and can be described as TGF-beta antagonists and/ or BMP-antagonists. This polypetide sequence is a bone morphogenetic protein receptor type 1 given in an exemplification of the invention.
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                                                                                     ; bone morphogenetic protein; bone injury; antibody production; antagonist; BMP-antagonist; osteopathic; osteopenias;
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100.0%; Pred. No. 8.6e-279;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                             16-JUN-2003; 2003US-00463190
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                 07-APR-2005 (first entry)
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4atches 532; Conservative
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Winkler DG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor; bone morphogenetic protein; bone injury; antibody production; TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG
             241 GKGRYGEVMAGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG
                                                        SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAH
                                                                        HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR
                                                                                                                                                                                          New antibody or antigen-binding fragment that binds specifically to sclerostin polypeptide and which inhibits binding of sclerostin polypeptide to a bone morphogenic protein, useful for increasing bone mineral content or density.
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Winkler D
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and other disorders related to low bone mineral content and density. As such, these compositions improve bone mineralization and can be described as TGF-beta antagonists and/ or BMP-antagonists. This polypeptide sequence is a bone morphogeneric protein receptor type I given in an exemplification of the invention.
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                                                                                                            100.0%; Score 2838; DB 9;
100.0%; Pred. No. 8.6e-279;
ive 0; Mismatches 0;
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ADX97416 standard; protein; 532 AA.

RESULT 8 ADX97416 ADX97416;

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This invention relates to a novel antibody or antigen-binding fragment that binds specifically to a sclerostin (SOST) polypeptide and impairs formation of a sclerostin homodimer. Specifically, it refers to an antibody that competitively inhibits binding of the sclerostin cantibody that competitively inhibits binding of the sclerostin cantibody that competitively inhibits binding of the sclerostin compensation or a BMP Type II receptor binding site. The present invention can secribe a hybridoma cell capable of producing the antibody and a host cell for antibody expression. Furthermore, it provides a nucleic acid molecule encoding a transforming growth factor-beta (TGF-beta) binding protein known as SOST (and also BEER) and methods for detection thereoff. Accordingly, such antibodies and osteopathic compositions of the invention can be used for treating osteopenia, osteoporosis, fractures and other disorders related to low bone mineral content and density. As such, these compositions improve bone mineralization and can be described sequence is a bone morphogenetic protein receptor type I given in an exemplification of the invention.
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100.0%; Pred. No. 8.6e-279;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 110; 205pp; English.
(CLLT ) CELLTECH R & D INC.
                                                              Galas DJ, 1
Winkler DG;
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Matches 532, Conserv
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The invention relates to a novel isolated antibody, or its antigenbinding fragment, which binds specifically to a sclerostin (SOST)

Colypeptide. The SOST polypeptide comprises any of 6 sequences having 190

or 213 amino acids, fully defined in the specification (DAD97341,

Competitively inhibits binding of the SOST polypeptide to a bone

morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II

Receptor binding atte, where the BMP Type I Receptor binding site is

morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II

Receptor binding to a BMP Type I Receptor binding site is

capable of binding to a BMP Type I Receptor binding site is

capable of binding to a BMP Type I Receptor binding site is

capable of binding to a BMP Type I Receptor binding site is

call that is capable of expressing the new antibody; a composition

cult that is capable of expressing the new antibody; a composition

cult that is capable of expressing to antibody; a composition and post site of physiological carrier; an immunogen comprising a peptide comprising 6, 7,

call that is capable of expressing the new antibody that specifically binds to the SOST polypeptide; and methods for identifying an antibody

che SOST polypeptide; methods for producing an antibody that specifically binds to the SOST polypeptide, and methods for identifying an antibody

chat impairs binding of a BMP to the SOST polypeptide, that impairs SOST condimer formation, or that increases bone mineral content. The novel antibody and compositions have osteopathic activity. The SOST nucleic acids may be used in gene therapy. The composition and methods are useful for increasing bone mineralization, which may treat or prevent diseases

cor conditions associated with low bone mineral density, such as

cort conditions associated with low bone mineral density, such as

cort conditions associated with low bone faractures. This sequence represents a

cort conditions associated by the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated antibody specific for a sclerostin polypeptide, useful for increasing bone mineralization or for treating or preventing conditions associated with low bone mineral density, e.g. osteoporosis or
                                                                                                                                                                     antibody; sclerostin; SOST; bone morphogenic protein receptor;
Transforming Growth Factor; osteopathic; gene therapy; bone repair;
                                                                                                                       Rat bone morphogenic protein type I receptor, SEQ ID 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 76; 157pp; English.
                                                                                                                                                                                                                            osteopenia; osteoporosis; bone injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Latham J;
                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2004; 2004WO-US018912.
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1 MTQLYTYIRLLGACLFIISHVQGQNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLK

100.0%; Score 2838; DB 9; Length 532; 100.0%; Pred. No. 8.6e-279; ive 0; Mismatches 0; Indels 0;

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Similarity

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Query Match

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PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKWVESQDVKI

PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESODVKI

RDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKN HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR

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CYCSGHCPDDAINNTCITNGHCFAIIEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR
                                                                                    121 TIECCRINLCNOYLOPTLPPVVIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYC
                                                                                                   TIECCRINLCNQYLQPTLPPVVIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYC
                                                                                                                                   KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
                                                                                                                                                     KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
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Transforming Growth Factor; osteopathic; gene therapy; bone repair;
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The invention relates to a novel isolated antibody, or its antigenbinding fragment, which binds specifically to a sclerostin (SOST)

CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190 or 213 amino acids, fully defined in the specification (ADX97341, ADX97360, ADX97389, ADX97400, ADX97402 or ADX97408). The antibody competitively inhibits binding of the SOST polypeptide to a bone competitively inhibits binding of the SOST polypeptide. The antibody competitively inhibits binding of the SOST polypeptide. The invention capable of binding of a BMP Type I Receptor binding site and a BMP Type I Receptor binding site is capable of binding to a BMP Type I Receptor binding site is capable of expressing the new antibody; a composition to a manufactor of comprising the new antibody; a composition to a comprising the new antibody, a composition of a physiological carrier; an immunogen comprising a peptide comprising 6, 7, comprising the new antibody, or its antigen-binding fragment, and a physiological carrier; an immunogen compressing a peptide comprising 6, 7, comprising to the SOST polypeptide; and methods for identifying an antibody that specifically binds to the SOST polypeptide; and methods for identifying an antibody chat modulates a Transforming Growth Factor (TGF)-beta signaling patkway, that impairs binding of a BMP to the SOST polypeptide, that impairs content. The novel conditions associated with low bone mineral density, such as accompania, osteoporosis or bone fractures. This sequence represents a concentry of the invention.
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100.0%; Pred. No. 8.6e-279;
ive 0; Mismatches 0;
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ADX97414 standard, protein; 532

RESULT 10 ADX97414 ID ADX9 CYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120

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The invention relates to a novel isolated antibody, or its antigen-
binding fragment, which binds specifically to a sclerostin (SOST)

CD polypeptide. The SOST polypeptide comprises any of 6 sequences having 190

or 213 amino acids, fully defined in the specification (ADX97341,

CD CANS97360, ADX97398, ADX97400, AXX97402 or ADX97408). The antibody

CC competitively inhibits binding of the SOST polypeptide to a bone

morphogenic protein (BMP) Type I Receptor binding site is

CC Capable of binding site, where the BMP Type I Receptor binding site is

CC Capable of binding to a BMP Type I Receptor binding site is

CC Capable of binding to a BMP Type I Receptor binding site is

CC Capable of binding to a BMP Type I Receptor binding it and a bone

CC capable of binding to a BMP Type I Receptor polypeptide. The invention

CC capable of binding to a BMP Type I Receptor polypeptide. The invention

CC capable of binding to a BMP Type I Receptor polypeptide comprising 6, 7,

CC capable of binding to a BMP Type I Receptor polypeptide comprising 6, 7,

CC binds to the SOST polypeptide; and methods for identifying an antibody that specifically that impairs binding of a BMP to the SOST polypeptide, that impairs SOST homodimer formation, or that increases bone mineral content. The novel antibody and composition and methods are useful for increasing bone mineralization, which may treat or prevent diseases

CC conditions associated with low bone mineral density, such as a concention or become an or conditions as secondated with become an ineral capable.

CC concentration as a proposed by the composition and methods as a concention or become mineral density, such as a secondated with low bone mineral capable.

CC concentration or because the may be a secondated with low bone mineral capable.

CC concentration or because the may be a secondated with low bone mineral capable.

CC concentration or concentration or conditions are useful concentrations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated antibody specific for a sclerostin polypeptide, useful for increasing bone mineralization or for treating or preventing conditions associated with low bone mineral density, e.g. osteoporosis or
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                                                                                                                                                                  terostin; SOST; bone morphogenic protein receptor; Growth Factor; osteopathic; gene therapy; bone repair;
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100.0%; Pred. No. 8.6e-279;
ive 0; Mismatches 0;
                                                                                                                                                                                                                  osteopenia; osteoporosis; bone injury.
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                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2004; 2004WO-US018912
                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-2003; 2003US-0478977P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CLLT ) CELLTECH R & D INC.
                                                                        (first entry)
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532; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADX97428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 532 AA;
                                                                                                                                                                                                                                                                                                                 WO2005014650-A2
                                                                                                                                                                                                Pransforming
                                                                      05-MAY-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Winkler DG,
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                                                                                                                                                                                                                                                                 Rattus sp.
                                                                                                                                                                     antibody;
                         ADX97414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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241 GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWPRETEIYQTVLMRHENILGFIAADIKGTG 300
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                                                                                                                                                                                                                                                                                                                                        480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated antibody, or its antigen-bidding fragment, which binds specifically to a sclerostin (SOST) polypeptide comprises any of 6 sequences having 190 or 213 amino acids, fully defined in the specification (ADX97341,
                                                                                                                                                                                                                                                  RDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKN 420
                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                            HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated antibody specific for a sclerostin polypeptide, useful for increasing bone mineralization or for treating or preventing conditions associated with low bone mineral density, e.g. osteoporosis or
                                                                                   KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
                                                                                                                                                                                         SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAH
                                                                                                                                                                                                                                                                   RDLKSKNILLIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKN
                                                                                                                                                                                                                                                                                                                              KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
                                                                                                                             GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETE1YOTVLMRHEN1LGF1AAD1KGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; sclerostin; SOST; bone morphogenic protein receptor;
Transforming Growth Factor; osteopathic; gene therapy; bone repair;
                                                                                                                                                                                                                                                                                                                                                                       532
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                                                                                                                                                                                                                                                                                                                                                                     PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKWVESQDVKI
                                                                                                                                                                                                                                                                                                                                                                                      PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat bone morphogenic protein type Ia receptor, SEQ ID 79.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADX97419 standard; protein; 532 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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1 MTQLYTYIRLLGACLFIISHVQGQNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLK 1 MTQLYTYIRLLGACLFIISHVQGQNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLK

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competitively inhibits binding of the SOST polypeptide to a bone morphogenic protein (BMP) Type I Receptor binding site is a Receptor binding site; where the BMP Type I Receptor binding site is capable of binding to a BMP Type I Receptor polypeptide. The invention further comprises: a hybridoma cell producing the new antibody; a host cell that is capable of expressing the new antibody; a composition comprising the new antibody, or its antigen-binding fragment, and a physiological carrier; an immunogen comprising a peptide comprising 6, 7, 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acide of the SOST polypeptide; methods for producing an antibody that specifically consider methods for producing an antibody that specifically that modulates a Transforming Growth Factor (TGP)-beta signaling pathway, that impairs binding of a BMP to the SOST polypeptide, that impairs SOST canding of a BMP to the SOST polypeptide, that impairs SOST canding of a BMP to the SOST polypeptide, that impairs SOST canding of a BMP to the SOST polypeptide, that impairs SOST canding an antibody and compositions have osteopathic activity. The SOST nucleic acted may be used in gene therapy. The composition and methods are useful for increasing bone mineralization, which may treat or prevent diseases or conditions associated with low bone mineral density, such as secondarial and processing a receptor of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 2838; DB 9; 100.0%; Pred. No. 8.6e-279;
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standard; protein; 532

AAR74343

AAR74343

(revised)
(first entry)

25-MAR-2003 01-NOV-1995

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New bone morphogenetic protein receptor kinase protein - used for identifying cpds. capable of binding it and for developing therapeutic cpds. and detection system(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A cDNA library prepared from NIH3T3 poly-A RNA was screened with J159 fragment to isolate clone BRK-1 (sequence given in AAQ90184) encoding full-length BMP receptor kinase protein (AAR74343). Vectors including DNA were used to express recombinant BRK-1 in CHO and COS-7 hosts. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTQLYTYIRLLGACLFIISHVQGQNLDSMLHGTGMKSDLDQKKPENGVTLAPEDTLPFLK
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                           BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein.
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                                                                                                                                        Extracellular ligand binding domain
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                                                                                                                                                                               177. .532
/label= Intracellular_kinase_domain
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Pred. No. 2.9e-277;
5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                     Rosenbaum JS,
                                                                                                                        24. .152
/label= Extracellular_ligand
153. .176
/label= Transmembrane_domain
                                                                                               1. .23
/label=_Sig_peptide
                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 29-32; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                     Koenig BB,
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by monitoring reporter gene expression
                             Sequence 532 AA;
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                           420
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RDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKN
              361 RDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTKRYMAPEVLDESLNKN
                                                     HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNWVPSDPSYEDMREVVCVKRLR
                                                                                421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR
                                                                                                                                                                                                                                                                                                                    Mouse; bone morphogenetic protein receptor kinase-1; bone morphogenetic protein receptor kinase-3; antibody; diagnostic; bone morphogenetic protein-agonist; drug screening; reporter gene; bone morphogenetic protein-agonist; hormone-responsive element.
                                                                                                              532
                                                                                                                           PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKWESQDVKI
                                                                                                        PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKNVESQDVKI
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                                                                                                                                                                                                                                                                                           Bone morphogenetic protein type-I receptor kinase-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   216. .221
/note= "Conserved BRK-1 motif"
398. .421
/note= "Peptide used to raise a
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I receptor kinase; BRK-1; BMP receptor.
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99.5%; Score 2823; DB 2;
98.9%; Pred. No. 2.9e-277;
iive 5; Mismatches 1;
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                                     Conservative
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05-JUN-1995;
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                                                                                               Full-length mouse bone morphogenetic protein (BMP) type I receptor kinase protein-1 (BRK-1) (AAR95225) is a receptor capable of binding BMP and transducing a signal initiated by the binding. Its amino acid sequence was deduced from a cDNA clone (AAT28021). A BMP receptor kinase protein complex formed of full-length, incomplete or soluble BMP type I receptor kinase protein and full-length, incomplete or soluble BMP type II receptor receptor kinase-3 (BKK-3) (see also AAR95222-24 and AAR95226-34) is useful for screening cpds. for BMP receptor affinity or for determining the concentration of a BMP receptor ligand in a clinical sample. The concentration of a BMP receptor ligand in a clinical sample. The complex can be expressed by host cells co-transfected with vectors carrying the appropriate DNA sequences (see also AAT28018-30)
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                                    Assays for bone morphogenetic protein activities - using complex of E
type I receptor kinase protein and BMP receptor kinase protein BRK-3.
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                                                                         Claim 2; Page 66-67; 101pp; English
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This represents a mouse BMP receptor kinase protein (BRK)-1. This can be used in the method of the invention of determining whether a compound can bind to a bone morphogenetic protein (BMP) receptor kinase protein complex. The method comprises allowing a compound in a sample to bind to the complex, where the complex is comprised of (i) a BMP; (ii) a BRK protein; (iii) an ActRIIB receptor. The method can be used to determine the concentration of a BMP receptor ligand in a sample by comparing the binding to a standard curve prepared with known concentrations of BMP ligand. The method can also be used to determine whether a test compound produces a signal on binding to a BMP receptor protein complex. The method is useful for determining whether a ligand, such as a known or putative drug, can bind to and/or activate the receptors
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BMP receptor kinase; ActRIIB receptor;
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Pred, No. 2.9e-277;
5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 88-91; 110pp; English
      BMP;
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Best Local Similarity 98.9%;
Matches 526; Conservative
   Bone morphogenetic protein;
BRK; receptor ligand; drug.
                                                                                                                                                                                                                                                                                                                                                                                                   & GAMBLE
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N-PSDB; AAV71972.
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                                                                                                                                                                                                                                                                                                                                                                                                          (PROC ) PROCTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosenbaum JS;
                                                                                                                                                       WO9852038-A1
                                                                                                                                                                                                                                                                                                                                            16-MAY-1997;
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481 PIVSNRMNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI 532	SNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI 532
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Search completed: December 3, 2005, 06:07:43 Job time : 193 secs

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1 MTQLYTYIRLLGACLFIISHVQGQNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLK
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 530
ATTONNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REGISTRATION NUMBER: 32,618
TELEFRANCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEFRANCE 617 876 1170
TELEFRANCE GIT 876 1170
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
CITY: Cambridge
US-08-436-265-18
US-09-679-187-18
US-09-2448-371A-8
US-09-2448-371A-8
US-09-344-015-18
US-09-349-016-10396
US-09-874-10396
US-09-874-10080-10
US-09-874-10080-10
US-09-349-016-9766
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US-09-679-187-10
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APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
APPLICANT: THIES, R. Scott
APPLICANT: TAMAJI, No. 6291206oru
TITLE OF INVENTION: RECEPTOR PROTEINS
INTHER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08123934A; Patent No. 6291206
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US-08-123-934A-2
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Sequence 12, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 6, Appli
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Sequence 4, Ap
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Sequence 18,
Sequence 18,
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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-382-256-14
US-08-158-175A-4
US-08-35-115-14
US-08-34-179A-12
US-08-34-179A-12
US-09-267-963D-14
US-09-267-963D-14
US-09-392-256-6
US-09-395-115-6
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US-08-158-735A-2
US-08-123-934A-4
US-09-874-628-4
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Maximum DB
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BR Floppy disk
COMPUTER: BREATIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US94/10080
FILING DATE: HEREWITH
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 17-SEP-1993
                                                                                                                          100.0%; Score 2838; DB 2;
100.0%; Pred. No. 8.6e-261;
ive 0; Mismatches 0;
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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-874-628-2
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GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.-
TYPE: amino acid
                                                                                                                                                 Local Similarity 100.
nes 532; Conservative
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PCT-US94-10080-2
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CYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
                                                                                TIECCRINLCNQYLQPTLPPVVIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYC 180
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                        CYCSGHCPDDAINNTCITNGHCFAIIEBDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR
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CELESTE, Anthony J.
THIES, R. Scott R. Scott R. Scott VAMAJI, NO. 6610513oru
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: ADDRESSEE Genetics Institute Inc.- Legal Affairs STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/W8-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/09/874,628
FILING DATE: 05-Jun-2001
CLASSIFICATION: <Unknown>
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REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Patent No. 6610513
GENERAL INFORMATION:
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US-09-874-628-2
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                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224657.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 931047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 33, 1993
APPLICATION NUMBER: 33, 1993
APPLICATION NUMBER: 33, 1993
APPLICATION NUMBER: 31, 1993
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
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Pred. No. 2.3e-259;
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98.9%; Pred. No. ...
5; Mismatches
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                                                                                                                        COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-382-256-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: NO. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 532 amino acide TYPE: amino acid
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                                                                                                                                                                                                                                            CLASSIFICATION: 514
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 SWIQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAH 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDLKSKNILLIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKN 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
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TEN DIJKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES,
AND THEIR USE
AND THEIR USE
                                                                                                                                                                                                                                                                                                   8; DB 4;
8.6e-261;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
                                                                                                                                                                                                                                                                                               100.0%; Score 2838;
ilarity 100.0%; Pred. No. 8.6
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09382256A Patent No. 6207814 GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: LAZAK, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203-
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 498-8261
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
                                                                                                                                                                                                                                MOLECULE TYPE: protein PCT-US94-10080-2
                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                   Matches 532;
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Best Local
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Gaps ö

Indels

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GENERAL INFORMATION:
APPLICANT: Miyazono, Kohel; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                       301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAH 360
                                                                                                                                                                                                                                                                                                        421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNWVPSDPSYEDMREVVCVKRLR 480
                                                                                                                                KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
                                                                                                                                                                                               SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAH
                                                                                                                                                                                                                                                                                    RDLKSKN1L1KKNGSCC1ADLGLAVKFNSDTNEVD1PLNTRVGTRRYMAPEVLDESLSKN
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2.1P: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PC7/0893/02367
FILING DATE: 17-No. 6271365ember-1993
PRIOR APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1993
PRIOR APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
APPLICATION NUMBER: 9304680.3
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Patent No. 6271365
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RIGARIOR APPLICATION DATA:
APPLICATION NUMBER: 9113763.6
FILING DATE: 2-UUIY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Ly
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US-09-395-115-14
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                                                                                                                                                    HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
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301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAH 360
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                                          RDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKN
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                                                                                                                                                                                                                     532
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COOK. JONATHAN S. APPLICANT: COOKEA, PAUL E. APPLICANT: COOKEA, PAUL E. APPLICANT: COREA, PAUL E. APPLICANT: ROSENGHUM, JAN S. APPLICANT: ROSENGHUM, JAN S. APPLICANT: TING, BETH B. APPLICANT: TING, SERRY TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: ADDRESSEE: THE PROCTER & GAMBLE COMPANY STREET: 11810 EAST MIAMI RIVER ROAD CITY: ROSS
CITY: ROSS
STATE: OH
COUNTRY: USA
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ZIP: 45061
ZIP: 45061
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: Plopy disk
COMPUTER: TBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/08/158,735A
FILING DATE: 24-NOV-1993
CLASSIFICATION: BATA:
APPLICATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 5088
TELEPHONE: (513) 627-2858
TELEPHONE: (513) 627-2858
TELEPHONE: (513) 627-2858
TELEPHONE: (513) 627-2866
; INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2823; DB 2;
Pred. No. 2.3e-259;
5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08158735A
Patent No. 6248554
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.9%;
Matches 526; Conservative
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US-08-158-735A-4
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61 CYCSGHCPDDAINNTCITNGHCFAIIEEDDGGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTQLYTYIRLLGACLFIISHVQGQNLDSMLHGTGMKSDLDQKKPENGVTLAPEDTLPFLK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/334,179A
FILING DATE: 04-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
99.5%; Score 2823; DB 2;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1;
                                                                                                                                                                                           FILING DATE: 04-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CORSTANGE, BRAHM J.
REGISTRATION UNMERR: 34,804
REFERENCE/DOCKET NUMBER: 5473
TELEPATON: 513-627-2858
TELEPATON: 513-627-2858
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08436265; Parent No. 6316217; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 532 amino acide
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-334-179A-12
                COUNTRY: US
ZIP: 45061
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-436-265-14
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                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.5%; Score 2823; DB 2; Length 532; Best Local Similarity 98.9%; Pred. No. 2.3e-259; Matches 526; Conservative 5; Mismatches 1; Indels
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PEPLICANT: NOHNO, TSUTOMU
TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
STREET: 11810 BAST MIAMI RIVER ROAD
          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9323344.5
FILING DATE: 15-OCCOBE-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOHIE!, VINEET
REGISTRATION NUMBER: 37,003
REFENCE/DOCKET NUMBER: LUD 529
TELEPAN: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPAN: (212) 688-9200
INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08334179A
Patent No. 6306622
GENERAL INFORMATION:
DATE: 3-August-1993
                                                                                                                                                                                                                                                       LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-09-395-115-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ROSS
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US-08-334-179A-12
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Sequence 14, Application US/09679187

Factont No. 6331621

GENERAL INFORMATION:

APPLICANT: Miyazono, Kohei, Dijke, Peter Ten;

APPLICANT: Miyazono, Kohei, Dijke, Peter Ten;

APPLICANT: Franzen, Petra; Yamashita, Hidetoshi, Heldin, Carl-Henrik

TITLE OF INVENTION: Activin Receptor-Like Kinase Domains And Their Use

TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 80s Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                  KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV 240
                                                                                                                                                                       241 GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG 300
                                                                                                                                                                                                                                                                         301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAH 360
                                                                                                                                                                                                                                                                                                                                                                                                                                    421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
PRIOR DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621ember-1992
PRIOR APPLICATION NUMBER: 9304677.9
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
APPLICATION NUMBER: 9304680.3
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-0CT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
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FILING DATE: 28-May-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
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APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;

APPLICANT: Franzon, Petra; Yamashita, Hideloshi; Heldin, Carl Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CYCSGHCPDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-NO. 6316217ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-NO. 6316217ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 6704677.9
FILING DATE: 6704680.3
PRIOR APPLICATION DATA: 7004680.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 8-MARCH-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 911047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 3-August 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 932134.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 amino acids
amino acid
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Matches 526; Conservative
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                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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Patent No. 5863738
GENERAL INFORMATION:
APPLICANT: TEN DIJKE, Peter
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohei
APPLICANT: MIYAZONO, Kohei
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Worphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         Score 2823; DB 2;
Pred. No. 2.3e-259;
5; Mismatches 1;
CURRENT FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/GB93/02367
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.2
LENGTH: 532
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STREET: 125 High St.
                                                                                                                                                                                                                                                         99.5%;
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.9
Matches 526; Conservative
                                                                                                                                                                           TYPE: PRT ORGANISM: Mus musculus
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US-08-481-337A-6
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Patent No. 6692925
GENERAL INFORMATION. Kohei
APPLICANT: IMAMURA, Takeshe
APPLICANT: INFORMATION. PROTEINS HAVING SERINE/THREONINE KINASE DOWAINS, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE
FILE REPERENCE: LUD 5539.1 CIP
CURRENT APPLICATION NUMBER: US/09/267,963D
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            FILING DATE: 3-Adgust 1993

FILING DATE: 3-Adgust 1993

APPLICATION DATA:
APPLICATION NUMBER: 9121344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vinee
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 888-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARATERISTICS:
APPLICATION NUMBER: 9136099.2
                                                                                                                                                                                                                                                                          LENGTH: 532 amino acids TYPE: amino acid
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US-09-267-963D-14
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COMPUTER READABLE FURG:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 02-UN-1995
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Thomas C.
REGISTRATION NUMBER: CRP-097CP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
INFORMATION FOR EQ ID NO: 6:
SEQUENCE CRARACTERISTICS:
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'SWAWMATION FOR EQ ID NO: 6:
'SWAWMATION ACIDS
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97.2%; Pred. No. 3.1e-254;
tive 7; Mismatches 8;
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amino acid
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Matches 517; Conservative
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MOLECULE TYPE: protein
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Sequence 6, Application US/09382256A Patent No. 6207814 GENERAL INFORMATION:

RESULT 12 US-09-382-256-6 APPLICANT: MIYAZONO, Kohei TEN DIJKE, Peter FRANZEN, Petra

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KSISSRGRYNRDLEQDEAFIPVGESLKOLIDQSQSSGSGCLPLLVQRTIAKQIQMVRQV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TIECCRINICNOYLOPTLPPVVIGPFPDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRINT APPLICATION DATA:
APPLICATION DATE: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 91937.6
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: AUJY 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: AUJY 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: AUGHS 7, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: AUGHS 7, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: AUGHS 7, 1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.6%; Score 2769; DB 2; Best Local Similarity 97.2%; Pred. No. 3.1e-254; Matches 517; Conservative 7; Mismatches 8;
                                                                                 NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: LUD 5298.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 752-5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 532 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Sequence 6, Application US/08436265

Sequence 6, Application US/08436265

Patent No. 6316217

GENERAL INFORMATION:

APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;

APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik

TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins

TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

STREET: New York City

ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GKGRYGEVWMGKWRGEKVAVKVPFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGGGLPLLVQRTIAKQIQMVRQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                            97.6%; Score 2769; DB 2; 97.2%; Pred. No. 3.1e-254; Live 7; Mismatches 8;
                                                      NAME: Kohlei, Vineet
REGISTATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFRA: (212) 888-9200
TELEFRA: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
                      ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 97.2
Matches 517; Conservative
                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-395-115-6
                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                       TYPE: amin
TOPOLOGY:
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Patent No. 6271365
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue CITY: New York City
                                                      GKGRYGEVWAGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG 300
                                                                                                                                                                                          KSISSRRRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSLPLLVQRTIAKQIQMVRQV 240
                                                                                                          241 GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG 300
                                                                                                                                                              SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAH 360
                                                                                                                                                                                                                                                                           RDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKN 420
                                                                                                                                                                                                                                                                                                                                                                                  421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION
APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6271365ember-1993
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1992
PRIOR APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION NUMBER: 931047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION NUMBER: 9311047.6
FILING DATE: 2-July-1993
PRIOR APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
FILING DATE: 3-AUGUST-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
OPTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/395,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-395-115-6
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Sequence 6, Application US/09679187

Patent No. 6331621

GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York City
      361 RDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDVPLNTRVGTKRYMAPEVLDESLNKN
                                                                   RDLKSKN1L1KKNGSCC1ADLGLAVKFNSDTNEVD1PLNTRVGTRRYMAPEVLDESLSKN
                                                                                                                                                 HFQPYIMADIYSFGLIIWEMARRCIITGGIVEEYQLPYYNWVPSDPSYEDMREVVCVKRLR
                                                                                                                                                                             421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNNVPSDPSYEDMREVVCVKRLR
                                                                                                                                                                                                                             481 PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI
                                                                                                                                                                                                                                                       PI VSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKWVESQDVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New rork
STATE: New York
SIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
"...nrmer: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFTWARE: Mordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-0CT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-0Ctober-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CB93/02367
FILING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LUD 5298
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 15-October-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 930466
FILING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                      US-09-679-187-6
                           301
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                         kb storage
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360
                                                                              SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kohlei, Vineet
REGISTRATION VUMBER: 37,003 2
REFERENCE/DOCKET NUMBER: LUD 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-3884
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
                                          COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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Best Local Similarity 97.21
Matches 517; Conservative
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                                                                                                                       Length 532;
                                                                                                                                               8; Indels
                                                                                                                   Query Match 97.6%; Score 2769; DB 2; Best Local Similarity 97.2%; Pred. No. 3.1e-254; Matches 517; Conservative 7; Mismatches 8;
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: TOPLOGY: linear
JODLOGY: linear
US-09-679-187-6
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Search completed: December 3, 2005, 06:22:39 Job time: 47 secs

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
CTY: Cambridge
STATE: MA
COUNTRY: USA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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100.0%; Score 2838; DB 3;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0;
US-10-169-051-2
US-10-169-051-4
US-10-044-716-14
US-10-286-152A-40
US-10-21-220-112
US-10-295-027-68
US-10-295-027-881
US-10-295-027-881
US-10-295-027-881
US-10-295-027-881
US-10-463-190-104
US-10-463-190-108
US-10-463-190-108
US-10-463-190-108
US-10-463-190-108
US-10-463-190-108
US-10-682-190-108
US-10-682-190-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09874628
Patent No. US20020137133A1
GENERAL INFORMATION:
GELESTE, Anthony J.
THIES, R. Scott
YAMAJI, No. US20020137133A10ru
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING CORRAGE PATENTH KELLEL SOFTWARE: PATENTA PAPLICATION DATA:
APPLICATION NUMBER: US/9/874,628
FILING DATE: 05-Jun-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/123,934
FILING DATE: 17-SEP-193
ATTONEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELECOMMUNICATION TO SEG 1170
TELECOMMUNICATION FOR SEG 1170
TELECOMMUNICATION OF 3551
INFORMATION FOR SEG 11 876 1170
TELECOMMUNICATION OF 3551
INFORMATION FOR SEG 11 876 1170
TELEPHONE: 617 876 1170
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  US-09-874-628-2
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Sequence 6, Appli
Sequence 53229, A
Sequence 53236, A
Sequence 172, App
Sequence 173, App
Sequence 53235, A
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Sequence 106, App
Sequence 107, App
Sequence 110, App
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Sequence 6, Appli
Sequence 71, Appl
Sequence 38, Appl
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Sequence 7
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2038
1 MTQLYTYIRLLGACLFIISH.....TALRIKKTLAKMVESQDVKI
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-450-763-53235
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US-10-463-190-107
US-10-463-190-110
US-10-668-197-74
US-10-868-497-75
US-10-868-497-75
US-10-903-068-14
US-10-903-068-14
US-10-903-068-6
US-10-903-068-6
US-10-153-217-2
US-10-286-152A-38
US-10-486-152A-38
US-10-486-152A-38
US-10-486-152A-38
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US-10-486-152A-38
US-10-486-152A-38
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US-10-745-237-308
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Maximum Match 100% .
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                      TIECCRINICNOYLOPTLPPVVIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYC 180
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Sequence 105. Application US/10463190

Publication No. US20040009535A1

GENEBAL INFORMATION:

APPLICANT: Brunkow, Mary E.

APPLICANT: Galas, David J.

APPLICANT: Mulligan, John T.

APPLICANT: Paeper, Bryan W.

APPLICANT: Wan Ness, Jeffrey

APPLICANT: Wan Ness, Jeffrey

APPLICANT: Winkler, David G.

TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR

TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR

TITLE OF INVENTION: COMPOSITIONS AND CURRENT APPLICANTON INVERSENCE 240083 508C2

CURRENT APPLICATION NUMBER: US/10/463,190

CURRENT FILING DATE: 2003-06-16

NUMBER OF SEQ ID NOS: 143

SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1e-243;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 532; Conservative 0
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US-10-463-190-105
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LENGTH: 532
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Publication No. US20040009535A1

GENERAL INFORMATION. Mary E.
APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
APPLICANT: Kovacevich, Brian
APPLICANT: Mulligan, John T.
APPLICANT: Walkler, David G.
TILE OF INVENTION: INCREASING BONE MINERALIZATION
FILE REFERENCE: 240083.508C2
CURRENT APPLICATION NUMBER: US/10/463,190
CURRENT FILING DATE: 2003-06-16
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FREESEQ for Windows Version 3.0
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iive 0; Mismatches 0
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Matches 532; Conservative
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US-10-463-190-106
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Sequence 110, Application US/10463190

Publication No. US20040009535A1

GENERAL INFORMATION:

APPLICANT: Galas, David J.

APPLICANT: Galas, David J.

APPLICANT: Wulligan, John T.

APPLICANT: Walkler, David G.

APPLICANT: Van Ness, Jeffrey

APPLICANT: Van Ness, Jeffrey

APPLICANT: Van Ness, Jeffrey

TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR

TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR

TITLE OF INVENTION: LOWERASING BONE MINERALIZATION

FILE REFERENCE: 240083.508C2

CURRENT APPLICATION NUMBER: US/10/463,190

CURRENT FILING DATE: 2003-06-16

NUMBER OF SEQ ID NOS: 143

SOFFWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 110

LENGTH: 532

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APPLICANT: Galas, David J.
APPLICANT: Galas, David J.
APPLICANT: Muligan, John T.
APPLICANT: Wulligan, John T.
APPLICANT: Paeper, Bryan W.
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
TITLE OF INVENTION: INCREASING BONE MINERALIZATION
FILE REPERENCE: 240083.508C2
CURRENT APPLICATION NUMBER: US/10/463,190
CURRENT FILING DATE: 2003-06-16
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FESTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 107, Application US/10463190; Publication No. US20040009535A1; GENERAL INFORMATION:
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ORGANISM: Rattus norvegicus
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Best Local Similarity 100.
Matches 532; Conservative
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US-10-463-190-107
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APPLICANT: Latham, John
TITLE OF INVENTION: ANTHODIES SPECIFIC FOR SCLEROSTIN AND
TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
FILE REFERENCE: 60117-128
CURRENT APPLICATION NUMBER: US/10/868,497
CURRENT FILING DATE: 2004-06-15
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1e-243;
; Mismatches 0
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100.0%; Pre
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Best Local Similarity 100.
Matches 532; Conservative
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US-10-868-497-74
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                     421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNWVPSDPSYEDMREVVCVKRLR
 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNWVPSDPSYEDMREVVCVKRLR
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STREET: 87 CambridgePark Drive
CITY: Cambridge
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; Pred. No. 1e-243;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIR Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/600,645
FILING DATE: 23-Unn-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                                                              APPLICANT: WOZNEY, John
CELESTE, Anthony J.
THIES, R. Scott
YAMAJI, Noboru
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALONNEL LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFRENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPAN: 617 876 1170
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
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Publication No. US20040142417A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;

Matches 532; Conservative 0
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US-10-600-645-2
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TYPE: PRT
ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Winkler, David G.
APPLICANT: Winkler, David G.
APPLICANT: Shi, Jiye
APPLICANT: Latham, John
TITLE OF INVENTION: METHODES SPECIFIC FOR SCI.
TITLE OF INVENTION: METHODS FOR INCREASING BON
FILE REPERBENCE: 60177-128
CURRENT APPLICATION NUMBER: US/10/868,497
CURRENT FILING DATE: 2004-06-15
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                 Sequence 75, Application US/10868497
Publication No. US20050106683A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Rattus norvegicus US-10-868-497-75
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Sequence 76, Application US/10868497
; Sequence 76, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Latham, John
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; FILE REFERENCE: 60117-128
; CURRENT PILIOR DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
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US-10-668-497-79

Sequence 79, Application US/10868497

Sequence 79, Application US/10868497

Publication No. US20050106683A1

GENERAL INFORMATION:

APPLICANT: Winkler, David G.

APPLICANT: Minkler, David G.

APPLICANT: Latham, John

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND

TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 532;
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Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/903,068
FILING DATE: 11-Jul-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: LUD TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                             NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 532 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.5%;
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Best Local Similarity 98.9
Matches 526; Conservative
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US-09-903-068-14
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Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
Having Serine Threonine Kinase Domains And Their Use
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                                                                                                                                                        Length 532;
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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                                                                                                                                                           DB 5;
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                                                                                                                                                                      1e-243;
                                                                                                                                                        i; Score 2838; Ei; Pred. No. 1e-20; Mismatches
; FILE REFERENCE: 60117-128
CURRENT APPLICATION NUMBER: US/10/868,497;
CURRENT FILING DATE: 2004-06-15
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 79
LENGTH: 532
TYPE: PRT
CORGANISM: Rattus Sp.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
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Patent No. US20020123139A1
GENERAL INFORMATION:
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Conservative 0;
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532; Conserv
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US-09-903-068-14
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Best Local S:
Matches 532
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APPLICATION NUMBER: 09/679,187

APPLICATION NUMBER: 07/6893/02367

FILING DATE: 4Unknowns

APPLICATION NUMBER: 927(5893/02367

FILING DATE: 17-No. US20020123139Alember-1993

APPLICATION NUMBER: 9204057,1

APPLICATION NUMBER: 9304677,9

FILING DATE: 14-No. US20020123139Alember-1992

APPLICATION NUMBER: 9304680,3

FILING DATE: 8-March-1993

APPLICATION NUMBER: 9311047.6

FILING DATE: 2-May-1993

APPLICATION NUMBER: 91136099.2

FILING DATE: 2-May-1993

APPLICATION NUMBER: 91136099.2

FILING DATE: 3-August-1993

APPLICATION NUMBER: 931244.5

FILING DATE: 3-August-1993

APPLICATION NUMBER: 9321344.5
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Pred. No. 2.2e-242;
5; Mismatches 1;
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APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
Franzen, Peterra; Yamaelita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
Having Serine Threonine Kinase Domains And Their Use
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FILING DATE: «Unknown»

APPLICATION NUMBER: PCT/GB93/02367

FILING DATE: 17-No. US20020123139Alember-1993

APPLICATION NUMBER: 9224057,1

FILING DATE: 17-No. US20020123139Alember-1992

APPLICATION NUMBER: 9304677,9

APPLICATION NUMBER: 9304680,3

FILING DATE: 8-March-1993

APPLICATION NUMBER: 9311047,6

FILING DATE: 2-3119-1993

APPLICATION NUMBER: 9313763,6

FILING DATE: 2-3119-1993

APPLICATION NUMBER: 9313763,6

FILING DATE: 3-Auguet-1993

APPLICATION NUMBER: 9313763,6

FILING DATE: 3-Auguet-1993
                                                                                                                                                                                                                                                                                                                                                 ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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Pred. No. 1.4e-237;
7; Mismatches 8;
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APPLICATION NUMBER: US/09/903,068
FILING DATE: 11.Jul-2001
PRIOR APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                             STREET: 805 Third Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect
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                                                                                                                                                                                                                                                            ADDRESSEE: Felfe & Lynch
                                                US/09903068
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TYPE: amino acid
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                                                                                                                                                                                                           NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                            ; Sequence 6, Application US;
; Patent No. US20020123139A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM
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Best Local S
Matches 517
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APPLICANT: MIYAZONO, Kohei
APPLICANT: MIYAZONO, Kohei
APPLICANT: MIYAZONO, Kohei
APPLICANT: DEN DIJUKE, PECET
TITLE OF INVENTION PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE
FILE REFERENCE: LUD 5539.1 CIP
CURRENT APPLICATION NUMBER: US/09/267,963
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/GB93/02367
PRIOR APPLICATION NUMBER: US 09/039,177
PRIOR FILING DATE: 1998-03-13
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                      PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI 532
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                                                                                                                                                          Sequence 14, Application US/10739413
Publication No. US20050048607A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
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Best Local Similarity 98.9
Matches 526; Conservative
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US-10-739-413-14
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LENGTH: 532
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TITLE OF INVENTION: BMPRIA INVOLVEMENT IN JUVENILE POLYPOSIS
FILE REFERENCE: IOWA:037US
CURRENT APPLICATION NUMBER: US/10/153,217
PRIOR APPLICATION NUMBER: 60/292,691
PRIOR FILING DATE: 2001-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.6%; Score 2769; DB 4; Length 5
Best Local Similarity 97.2%; Pred. No. 1.4e-237;
Matches 517; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/10153217; Publication No. US20030072758A1; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 532
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US-10-153-217-2
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Sequence 6, Application US/09982543A

Setemation US/020155500A1

GENERAL INFORMATION:

APPLICANT: Dijke, P.

APPLICANT: Sampath, K.

APPLICANT: Sampath, K.

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTION: US/09/982,543A

CURRENT APPLICATION NUMBER: US/09/982,543A

CURRENT APPLICATION NUMBER: 08/448,371

PRIOR APPLICATION NUMBER: 08/448,371

PRIOR FILING DATE: 1995-06-02

NUMBER: OF SEQ ID NOS: 15

SEQ ID NO 6

SEQ ID NO 6
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97.6%; Score 2769; DB 3;
Best Local Similarity 97.2%; Pred. No. 1.4e-237;
Matches 517; Conservative 7; Mismatches 8;
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ORGANISM: Homo sapiens
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US-10-420-192-8

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Sequence 8, Application US/10420192

Publication No. US2005026057941

GENERAL INFORMATION:
APPLICANT: Lin, Herbert Y.
APPLICANT: Wainberg, Kobert A.
APPLICANT: Wainberg, Kobert A.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: TGF-Beta Type Receptor CDNAS Encoded Products and Uses
TITLE OF INVENTION: TGF-Beta Type Receptor CDNAS Encoded Products and Uses
TITLE OF INVENTION: TGF-Beta Type Receptor CDNAS Encoded Products and Uses
TITLE OF INVENTION: TGF-Beta Type Receptor CDNAS Encoded Products
FILE REFERENCE: 0399-1086-022

CURRENT TAPPLICATION NUMBER: US 09/584,929

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 1994-09-23

PRIOR FILING DATE: 1994-09-23

PRIOR FILING DATE: 1994-09-23

PRIOR FILING DATE: 1994-09-23

PRIOR FILING DATE: 1991-10-31

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 8

LENGTH: 567
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19.8%; Score 561.5; DB 6;
Best Local Similarity 29.1%; Pred. No. 8.5e-46;
Matches 144; Conservative 104; Mismatches 195;
US-11-109-156-13

US-10-509-422-5

US-11-081-214-1158

US-11-046-668-2

US-11-109-156-12

US-11-109-156-11

US-11-099-691-7

US-11-113-424-22

US-11-113-424-22

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US-11-10-156-18

US-11-667-295-101

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Sequence 20, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 61, Appl
Sequence 183, Appl
Sequence 185, Appl
Sequence 1201, Appl
Sequence 59, Appl
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1: /cgn2_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
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US-11-109-156-21
US-11-186-283-2
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US-11-021-441-14
US-11-021-441-20
US-11-031-441-20
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                                       GenCore version
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TITLE OF INVENTION: NOVEL CARK PROTEIN AND NUCLEIC ACID MOLECULES AND USES TITLE OF INVENTION: NOVEL CARK PROTEIN AND NUCLEIC ACID MOLECULES AND USES TITLE OF INVENTION: THEREPOR PROTEIN AND NOVEL CARK PROTEIN AND NOVEL CARENT FILE OF INVENTION: THEREPOR CURRENT FILING DATE: 2005-07-21

CURRENT FILING DATE: 2005-07-24

PRIOR FILING DATE: 2003-07-24

PRIOR FILING DATE: 1999-12-11

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-12-10

SOFTWARE: PATENTIN VOICE: 2.0

SOFTWARE: PATENTIN VOICE: 2.0

SOFTWARE: PATENTIN VOICE: 2.0
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                                                                                                                                                                                                                                                                                          LKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKNHF 422
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                                                                                                                                                  |-| -| -| | | | | | | | | | | GDVMLGDYRGNKVAVKCIKNDATAQAFLAEASVMTQL-RHSNLVQLLGVIVEEKGG---L
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                                                                                                                        GEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTGSWTQL
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  Mismatches 116;
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Pred. No. 8.6e-16;
                                        ESLKDLIDQSQSSGSGSGL----PLLVQRTIA-
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  67;
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Best Local Similarity 25.9%;
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  Conservative
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  87;
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                                                                  229 STCANNINHNTELLPIELDTLVGKGRFAEVYKAKLKQNTSEQFETVAVKIFPYEEYASWK 288
                                        RETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDFLKCATLDTRALL 332
                                                                                                                        333 KLAYSAACGLCHLHTEIYGTQGKP--AIAHRDLKSKNILIKKNGSCCIADLGLAVKFNSD 390
                                                                                                                                              391 TNEVDIPLNTRVGTRRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIWEMARRCITGGIV 450
                                                                                                                                                                                                                                                                                       EEYQLPYYNMVPSDPSYEDMREVVCVKRLRPIVSNRWNSDECLRAVLKLMSECWAHNPAS 510
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN TITLE OF INVENTION: PHOSPHATASE FILE REFERENCE: 06501-099002 CURRENT APPLICATION NUMBER: US/11/109,156 CURRENT FILING DATE: 2005-04-19
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PRIOR FILING DATE: 2002-04-19
PRIOR PELLING DATE: 2002-01-29
PRIOR PELLING DATE: 2002-01-29
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PELLING DATE: 1999-10-18
PRIOR PELLING DATE: 2000-02-17
PRIOR PELLING DATE: 2000-02-17
PRIOR PELLING DATE: 2000-01-17
PRIOR PELLING DATE: 2000-01-11
PRIOR PELLING DATE: 2000-05-02
PRIOR PELLING DATE: 2000-05-02
PRIOR PELLING DATE: 2000-05-02
PRIOR PELLING DATE: 2000-05-02
PRIOR PELLING DATE: 2000-06-09
PRIOR PELLING DATE: 2000-06-09
PRIOR PELLING DATE: 2000-06-09
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Publication No. US20050250144A1
GENERAL INFORMATION:
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Shizuko Ishii
Tomoyasu Sugiyama
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25.4%;
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|||TAQCVAERFSEL 541
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APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
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SEQ ID NO 21
LENGTH: 450
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Tetsuji Otsuki
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US-11-109-156-21
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Best Local Similarity
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APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: DORTHOW, Daniel A., APPLICANT: DORTHOW, Daniel A., APPLICANT: DORTHOW, Daniel A., APPLICANT: DORTHOW, Daniel A., APPLICANT: COCK, David N.
TITLE OF INVENTION: EXCRAPISASION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: THEREOF TYLENG TO THE SET INVENTION: THEREOF TO THE SET INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: OF ORGANICAL OF ORGANIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 REKDGEFSVLQLVGMLRGIAAGMKYLANMNY-----VHRDLAARNILVNSNLVCKVS 236
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8.5%; Score 241.5; DB 7; Length 4
Best Local Similarity 24.4%; Pred. No. 1.5e-15;
Matches 97; Conservative 70; Mismatches 156; Indels
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US-11-021-441-18
Sequence 18, Application US/11021441
Publication No. US20050249748A1
GENERAL INFORMATION:
          494 RAVLKLMSECWAHNPAS 510
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724 CNV-ELMS-----PAS 733
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TITLE OF INVENTION: NOVEL CARK PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOR
FILE REFERENCE: MNI-068CP2
CURRENT APPLICATION NUMBER: US/11/186,283
CURRENT PILING DATE: 2003-07-21
PRIOR PELICATION NUMBER: US/10/626,173
PRIOR PELING DATE: 2003-07-24
PRIOR PELING DATE: 2003-07-24
PRIOR PELING DATE: 2001-09-05
PRIOR PELING DATE: 1099-12-11
PRIOR APPLICATION NUMBER: US 60/111,938
PRIOR APPLICATION NUMBER: US 09/291,839
PRIOR APPLICATION NUMBER: US 09/291,839
PRIOR APPLICATION NUMBER: US 09/458,457
PRIOR PELING DATE: 1999-04-14
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ 1D NOS: 9
456
                                                                                                                                                                                                                             457 YYNWVP----SDPSYEDMREVVCVKRLRPIVS----NRWNS-----DECLRAVLKLMSECW 504
                                                                                                                                                                                                                                                                          665 FAHLKPAAAADMAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKL-EECL 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    568 VDVAKGMEYLHSL---TQ---PIIHRDLNSHNILLYEDGHAVVADFGES-RFLQSLDEDN 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 YQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDFL--KCATLDTRALLKLA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 YSAACGLCHLHTEIYGTQGKPAJAHRDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVD 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYYNMVP----SDPSYEDMREVVCKRLRPIVS---NRWNS--------DECL 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :: | :| :| :| :| :| :| 664 PFAHLKPAAAADMAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVSKLEECL 723
                                                                                                                                          HINDERNAPEVETQCTRYT-----IKADVFSYALCLWEI----LTG-----EIP
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                                                                                                    397 PLNTRVGTRRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLP
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;; Pred. No. 3.2e-15;
65; Mismatches 112; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/11186283 Publication No. US20050255520A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.0%;
Matches 98; Conservative 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rattus norvegicus US-11-186-283-8
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LENGTH: 835
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US20050250144A1
                      GENERAL INFORMATION:
APPLICANT: Toshio Ota
APPLICANT: Takao Isogai
                                                                                                                                           Kaoru Otsuka
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SOFTWARE: PatentIn Ver. 3
                                                                                                                     Koji Hayashi
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Matches 84; Conserval
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APPLICANT:
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                                                                                                                             APPLICANT: DOBANA, includes W., Jr.
APPLICANT: DOBANA, includes W., Jr.
APPLICANT: LUCKETT, William S., Jr.
APPLICANT: LUCKETT, William S., Jr.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: UNMER: US 60/616,750
PRIOR FILING DATE: 2004-10-06
PRIOR FILING DATE: 2004-10-06
PRIOR FILING DATE: 2004-00-06
PRIOR FILING DATE: 2004-00-06
PRIOR FILING DATE: 2004-00-23
PRIOR FILING DATE: 2004-00-23
PRIOR FILING DATE: 2004-00-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 -- KCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAHRDLKSKNILLIKKNGSCCIA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 DLGLAVKFNSD-----TNEVDIPLNTRVGTRRYMAPEVLDESLSKNHFQPYIMA-DIYS 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   862 PCIVMWEV----MTYG-----BRPYWEL----SNHEVWKAINDGFRLPTPM-----D 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 -IDQSQSSGSGLPLLVQRTIAKQIQMVRQVGKGRYGEVWMG--KWRGEKVAVKVFFTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75; Gaps
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8.5%; Score 241.5; DB 7; Length 1035;
Best Local Similarity 24.4%; Pred. No. 4.8e-15;
Matches 97; Conservative 70; Mismatches 156; Indels 75;
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901 CPSAIYQLMMQCWQQERARPKFADIVSILDKLIRAPD 938
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                                         Sequence 4, Application US/11021441
Publication No. US20050249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: PORTNOY, Daniel A.
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US-11-109-156-17
; Sequence 17, Application US/11109156
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LENGTH: 1035
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231 AKQIQMVRQVGKGRYGEVWMGKWRGEKVAVKVFF----TTEEASWFRETEIYQTVLMRHE 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 CGLCHLHTEIYGTQGKPAIAHRDLKSKNILIKKNGSCCIADLGLA-VKFN-SDTNEVDIP 397
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APPLICANT: Chiaki Senon
APPLICANT: Chiaki Senon
APPLICANT: Chiaki Senon
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
TITLE OF INVENTION: NOVEL SENON
CURRENT APPLICATION NUMBER: US/11/109,156
CURRENT FILING DATE: 2005-04-19
PRIOR FILING DATE: 2005-04-19
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-06-03
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US-10-990-276-1
; Sequence 1, Application US/10990276
                                                                                                                                                                                                                                              Keiichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
                                                                                                          Jun-Ichi Yamamoto
                                                                                                                               Shizuko Ishii
Tomoyasu Sugiyama
Ai Wakamatsu
Tetsuo Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Conservative
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177 KHYCKSISSRGRYNRDLE-QDEAFIPVG----ESLKDLIDQSQSSGSGSGLPLLVQRTIA 231
                                                                                                                                                                                                                                        232 KOIOMVROVGKGRYGEVWMGKWRGEKVAVK----VFFTTEEASWFRETEIYQTVLMRHE 286
                                                                                                                                                                                                                                                                         287 N---ILGFIAADIKGTGSWTQLYLITDYHENGSLYDFLKC----ATLDTRALLKLAYSAA 339
                                                                                                                                                                                                                                                                                                                                                                                   244 NLVELLGF------SSDSDNLCLVYAYMPNGSLLDRLSCLDGTPPLSWHTRCKVAQGTA. 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 CGLCHLHTEIYGTQGKPAIAHRDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLN 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 TR-VGTRRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIWEMARRCITG-GIVEEYQLP 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 CFAIIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRRTIECCRTNLCNQYLQPTLPPV 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gangoll: et al.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: 06/256,704
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/311,613
PRIOR PILING DATE: 2001-08-20
PRIOR PILING DATE: 2001-08-20
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-07-24
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-29
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-29
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-29
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-19
                                                                                                                                                                                    142 EHSCEPPDSSSPDNRSVESSDTRFHSFSFHELKSITNNFDEQPASAGGN----
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                                Length 459;
                                                                                 40; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  522 CFQTLTDDDY-------KSELREQL----
                              8.1%; Score 230; DB 6;
29.1%; Pred. No. 1.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 60, Application US/11113424; Publication No. US20050260713A1; GENERAL INFORMATION:
                                                                                 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : PatentIn Ver. 2.1
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                                                   Best Local Similarity
Matches 87; Conserv
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                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 F-----SSDGDDLCLVYVYMPNGSLLDRLSCLDGTPPLSWHMRCKIAQGAANGINFLH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 TEIYGTQGKPAIAHRDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRR 406
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                                        APPLICANT: Wesche, Holger

APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
TITLE OF INVENTION: RAK-4: Compositions and Methods of Use
FILE REPRENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/10/990,276
CURRENT FILING DATE: 2004-11-15
PRIOR PELING DATE: 2004-11-15
PRIOR PILING DATE: 2001-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
SEQ ID NOS: 7
SOFWRAKE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.1%; Score 230.5; DB 6; Length 460; 28.4%; Pred. No. 1.7e-14;
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Fublication No. US2050255549A1
GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Tularik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
CURRENT APPLICATION NUMBER: US/10/990,276
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US/09/759,595
PRIOR APPLICATION NUMBER: US/09/759,595
PRIOR APPLICATION NUMBER: US/09/759,595
PRIOR PILING DATE: 2000-01-13
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Publication No. US20050255549A1
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Best Local Similarity 28.4%
...--hes 87; Conservative
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 91; Conserva
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                                  580 -----QHYSTGRGSPGMKIYIDPFTYEDPNEAVREFAKEIDVSFVKIEEVIGAGE 629
                                                                                                                                                                                                                     688 TKS----RPVMIITEFMENGALDSFLRQNDGQFTVIQLVGMLRGIAAGMKYLSEMNY--- 740
                                                                                                                                                                                                                                                                                                            296 IKGTGSWTQLYLITDYHENGSLYDFLK--CATLDTRALLKLAYSAACGLCHLHTEIYGTQ 353
                                                                                                                                                                                                                                                                                                                                                                                 411 EVLDESLSKNHFQPYIMA-DIYSFGLIWE------MARRCITGGIVEEYQLPYY 458
                                                                                                                                                                                                                                                                                                                                                                                                            | : : | | ::|:|| | 3.4 EAI-----AYRKFTSASDVWSYGIVMEVWSYGERPYWDMSNQDVINAIEQDYRLP-- 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 NMVPSDPSYEDMREVVCVKRLRPIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIK 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 PVVIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYCKSISSRGRYNRDLEQDEAF 199
--- QMVRQVGKGR 244
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                                                                                         245 YGEVWMGKWR--GEK---VAVKV----FFTTEEASWFRETEIYQTVLMRHENILGFIAAD
                                                                                                                                                                                                                                                                                     354 GKPAIAHRDLKSKNILLIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTR---RYMAP
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TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
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PRIOR APPLICATION NUMBER: 60/256,704
PRIOR APPLICATION NUMBER: 60/311,590
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR PELICATION NUMBER: 60/211,613
PRIOR PELICATION NUMBER: 60/311,613
PRIOR PELICATION NUMBER: 60/315,617
PRIOR PELING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-07-34
PRIOR PELING DATE: 2001-07-34
PRIOR PELING DATE: 2001-07-34
PRIOR PELING DATE: 2001-07-34
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-05-29
PRIOR PILING DATE: 2001-05-29
PRIOR PILING DATE: 2001-05-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 62, Application US/11113424
Publication No. US20050260713A1
GENERAL INFORMATION:
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Matches 98; Conservative
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ORGANISM: Gallus gallus
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876 NTLDKMIRN 884
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APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: DUBENSKY, Daniel A.
APPLICANT: LUCKETT, William S., Jr.
APPLICANT: COOK, David N.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: THEREOF FILE REFERENCE: 282172003900
                                                    -----EYTDKLQHYTSGHMTPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVI 636
                                                                                                                                                                                                                                                                                                            693 HLEGVVTKS----SPVMIITEFMENGSLDSFLRQNDGQPTVIQLVGMLRGIAAGMKYLAD 748
                                                                                                                                                                                                                                                                                                                                                                                                                                              749 MNY------VHRDLAARNILVNSNLVCKVSDFGLSRFLEDDTS--DPTYTSALGGKIP 798
                                                                                                                                                                                                                                                                                                                                                                                                       EIYGTQGKPAIAHRDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTR-- 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         406 -RYMAPEVLDESLSKNHFQPYIMA-DIYSFGLIIWEMARRCITGGIVEEYQLPYYNWVPS 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPSYEDMREVVCVKRLRPIVSNRWNSD-----ECLRAVLKLMSECWAHNPASRLTALR 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231
                                                                                                                                                                           GKGRYGEVWMG--KWRGEK---VAVKVF---FTTEEASWFRETEIYQTVLM---RHENIL
                                                                                                                                                                                                                                                                      290 GFIAADIKGTGSWTQLYLITDYHENGSLYDFLK--CATLDTRALLKLAYSAACGLCHLHT
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200 IPVGESLKDLIDQSQSSGSG---SGLPLLVQ------RTIAKQIQM----VRQV-
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CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: US 60/616,750
PRIOR FILING DATE: 2004-10-06
PRIOR PILING DATE: 2004-10-01
PRIOR PILING DATE: 2004-10-01
PRIOR PELING DATE: 2004-10-01
PRIOR PILING DATE: 2004-00-05
PRIOR PILING DATE: 2004-00-05
PRIOR PILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-07-23
PRIOR PILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-07-03-06
PRIOR FILING DATE: 2004-07-30
PRIOR FILING DATE: 2004-07-30
PRIOR FILING DATE: 2004-03-26
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/11021441 Publication No. US20050249748A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Fusion protein US-11-021-441-20
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APPLICANT: DOENTY, includes W., Jr.
APPLICANT: DOENTY, baniel M., Jr.
APPLICANT: DOENTY, baniel M., Jr.
APPLICANT: COCK, David N.
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TILLE REPERENCE: 281,7203,900
CURRENT APPLICATION NUMBER: US/11/021,441
CURRENT APPLICATION NUMBER: US 60/616,750
PRIOR FILLING DATE: 2004-10-06
PRIOR FILLING DATE: 2004-10-01
PRIOR FILLING DATE: 2004-0-06-05
PRIOR FILLING DATE: 2004-0-0-03
PRIOR FILLING DATE: 2004-0-0-23
PRIOR FILLING DATE: 2004-0-0-23
PRIOR FILLING DATE: 2004-0-0-23
PRIOR FILLING DATE: 2004-0-0-33
PRIOR FILLING DATE: 2004-0-0-30
PRIOR FILLING DATE: 2004-0-3-26
PRIOR FILLING DATE: 2004-0-3-26
|: ||| : : : : | | :::||| : : | | :::|| | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : : | | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                   352 TQGKPAIAHRDLKSKNILIKKNGSCCIADLGLAVKFNSD-----TNEVDIPLNTRVGTF: 405
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                                                                                                                                         295 DIKGT-GSWIQLYLITDYHENGSLYDFL--KCATLDTRALLKLAYSAACGLCHLHTEIYG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 RYMAPEVLDESLSKNHFQPYIMA-DIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSD 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 PSYEDMREVVCVKRL-RPIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAK 523
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7.8%; Score 222; DB 7; Length 49°
Best Local Similarity 24.3%; Pred. No. 1.2e-13;
Matches 89; Conservative 63; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 497
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US-11-021-441-22
Sequence 22, Application US/11021441
Publication No. US20050249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Ur.
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378 LIRAPD 383
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Sequence 26, Application US/11021441

GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: DORTNOY, Daniel A.
APPLICANT: COOK, Daniel A.
APPLICANT: COOK, Daniel A.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THERROF
FILE REFERENCE: 2817203390

CURRENT FILING DATE: 2004-12-23
FRIOR PELICATION NUMBER: US 60/616,750
FRIOR PELICATION NUMBER: US 60/616,750
FRIOR APPLICATION NUMBER: US 60/615,287
FRIOR APPLICATION NUMBER: US 60/615,287
FRIOR APPLICATION NUMBER: US 60/599,377
FRIOR FILING DATE: 2004-00-05
FRIOR FILING DATE: 2004-00-05
FRIOR FILING DATE: 2004-00-05
FRIOR FILING DATE: 2004-00-05
FRIOR FILING DATE: 2004-07-23
FRIOR RELING DATE: 2004-06-30
FRIOR FILING DATE: 2004-01-03-65
FRIOR FILING DATE: 2004-01-03-05
FRIOR FILIN
                                                                                     232 KQIQMVRQVGKGRYGEVWMG--KWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENIL 289
                                                                                                                                    | :: | |: | || || || || || GQFSHHNIIRLEGVISKYKPWMIITEYMENGALDKFLREKDGEFSVLQLYGMLRGIAAGM 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 PYYNMVPSDPSYEDMREVVCVKRL-RPIVSNRWNSDECLRAVLKLMSECWAHNPASRLTA 514
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7.8%; Score 222; DB 7; Length 490;
Best Local Similarity 24.3%; Pred. No. 1.2e-13;
Matches 89; Conservative 63; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Fusion protein
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US-11-021-441-24

Sequence 24, Application US/11021441

Publication No. US20050249748A1

GENERAL INFORMATION:
APPLICAMT: DUBENSKY, Thomas W., Jr.
APPLICAMT: DUBENSKY, Thomas W., Jr.
APPLICAMT: DUBENSKY, Thomas W., Jr.
APPLICAMT: DUCKETY, William S., Jr.
APPLICAMT: COOK, David N.
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 2004-12-23
FILE REFERENCE: 2004-12-23

PRIOR APPLICATION NUMBER: US 60/615,287

PRIOR FILING DATE: 2004-00-0

PRIOR FILING DATE: 2004-00-0

PRIOR PELING DATE: 2004-00-0

PRIOR FILING DATE: 2004-00-30

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

PRIOR PRILING DATE: 2004-07-36

PRIOR PRILING DATE: 2004-07-30

PRIOR PRILING DATE: 2004-07-30

PRIOR PRILING DATE: 2004-06-30

PRIOR PRILING DATE: 2004-06-30

PRIOR PRILING DATE: 2004-06-30

PRIOR PRILING DATE: 2004-07-30

PRIOR PRILING DATE: 2004-07-30
                                       186 RGRYNRDLEQ--DEAFIPVGESLKDL---IDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV 240
                                                                                                                              352 TQGKPAIAHRDLKSKNILJKKNGSCCIADLGLAVKFNSD-----TNEVDIPLNTRVGTR 405
                                                                                                                                                                                                                                                         406 RYMAPEVLDESLSKNHFOPYIMA-DIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSD 464
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                                                                                                                                                                                                                                                                                                                                                                                                                         333 SNHEVMKAINDGFRLPTPM-----DCPSAIYQLMMQCWQQERARRPKFADIVSILDK 384
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                                                                                                                                                                      247 -----VHRDLAARNILVNSNLVCKVSDFGLSRVLEDDPEATYTTSGGKIPI-----
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1 Similarity 24.3%; Pred. No. 1.2e-13;
89; Conservative 63; Mismatches 146; Indels
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                                                        PSYEDMREVVCVKRL-RPIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAK 523
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Search completed: December 3, 2005, 06:26:05 Job time : 13 secs

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OM protein - protein search, using sw model

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US-10-600-645-2
2838
1 MTQLYTYIRLLGACLFIISH.....TALRIKKTLAKMVESQDVKI 532 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	bone morphogenetic	bone morphogenetic	ALK-3 - human	BMP receptor precu	serine/threonine k	activin receptor-1	receptor protein k			transforming growt	activin receptor-1	receptor protein k	activin A receptor	ŭ	activin type I rec	transforming growt	activin A receptor	type I serine-thre	activin/TGF-beta-1	activin receptor 1	ALK-1 - mouse	Dpp receptor SAX p	activin type I rec		activin type I rec	hypothetical prote	recep	activin receptor S	activin receptor p
SUMMARIES	ID		A56238	137163	A54985	JC2491	A53444	A56683	JC2061	145713	JC2062	A49432	A56693	A45992	A55921	A49664	159576	I38859	153417	A49431	JC4337	148241	I45712	180182	180183	PC4260	T15734	JQ1317	н	A39896
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					23.2	20.7	20.6	20.6	20.4	20.3	20.3	20.3		20.3	20.3

ALIGNMENTS

-	RESULT 1 JC2387 bone morph	RESULT 1 J02387 bone morphogenetic protein type IA receptor precursor - rat
	C; Species: Rattus no C; Date: 20-Feb-1995 C. Accession: JC2387	C;Species: Rattus norvegicus (Norway rat) jate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004 Accession: 170387
	R;Takeda, Biochem B	RyTakeda, K.; Oida, S.; Ichijo, H.; Iimura, T.; Maruoka, Y.; Amagasa, T.; Sasaki, S. Biochem, Biochys, Res. Commun. 204, 203-209, 1994
	A, Title: MA, Referenc	A;Title: Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and A;Reference number: JC2387; MUID:95032096; PMID:7945360
	A;Accession: JC238/ A;Molecule type: mR A:Residues: 1-532 <	A;ACCEBBIOI: UC238/ Molecule type: mRNA A:Regiding: 1-512 <tak></tak>
	A; Cross-re	A;Cross-references: UNIPROT:Q64308; UNIPARC:UPI00000E8A68; DDBJ:D38082; NID:g1398909; P
	C;Keywords F;1-23/Dom	c;Aeywords: Air; glycoprotein; receptor; transmembrane protein F;1-23/Domain: signal sequence #status predicted <sig></sig>
	F;24-527/P	24-527/Product: bone morphogenetic protein type IA receptor #status predicted <bmp></bmp>
	F;232-528/Domain:	
	F;236-527/ F;240-248/ F;73/Bindi	7:245-527/Region: Kinase domain F;246-548/Region: protein kinase ATP-binding motif F;73/Binding site: carbohydrate (Asn) (covalent) #status predicted
	Query Match Best Local Matches 53	Query Match Best Local Similarity 100.0%; Pred. No. 8.7e-145; Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	ò	1 MTOLYTYIRLLGACLFIISHVOGONLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLK 60
	. A	
	ò	61 CYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
	qa	61 CYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLISGCMKYEGSDFQCKDSPKAQLRR 120
	ò	121 TIECCRTNLCNQYLQPTLPPVVIGPFPDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYC 180
	QQ	121 TIECCRTNLCNQYLQPTLPPVVIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYC 180
	λ̈́σ	181 KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGGLFLLVQRTIAKQIQMVRQV 240
	qq	181 KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV 240

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HFQPYIMADIYSFGL1IWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004
C;Accession: 137163; S37183
R;ten Dijke, P: Ichijo, H:; Franzen, P.; Schulz, P.; Saras, J.; Toyoshima, H.; Heldin, Oncogene B, 2879-2887
A;Title: Activin receptor-like kinases: a novel subclass of cell-surface receptors with A;Reference number: 137161; MUID:93390967; PMID:8397373
A;Accession: 137163
A;Accession: L37163
A;Accession: L37163
A;Accession: L37163
A;Reference number: Activin MUID:9330967; PMID:83973773
A;Reterence number: L37163
A;Reterence number: L37163
A;Reterence number: L37163
A;Residues: 1532 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
                                                                                                                                                                                                               KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI
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97.2%; Pred. No. 4.2e-141;
iive 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;232-528/Domain: protein kinase homology «KIN»
F;240-248/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 517; Conservative
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181

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Qy 241 GKGRYGEVWMCKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG 300 Db 241 GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG 300 Oy 301 SWTQLYLITDYHENGSLYDFLKCATLDFRALKLAYSAACGLCHLHTBIYGTQGKPAIAH 360 Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALKLAYSAACGLCHLHTBIYGTQGKPAIAH 360	
420 420 480 480	RESULT 5 JC2491 setine/threonine kinase receptor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 05-Oct-2004 C;Accession: JC2491 R;Yamaii, N; Celeste, A.J.; Thies, R.S.; Song, J.J.; Bernier, S.M.; Golt:man, D.; Lvon
KAVESQDVKI 532 KAVESQDVKI 532	Biochem. Biophys. Res. Commun. 205, 1944-1951, 1994 A;Title: A mammalian serine/threonine kinase receptor specifically binds BMP-2 and BMP-A;Reference number: JC2491; MUD:95110346; PMID:7811286 A;Accession: JC2491 A;Molecule ryne. mRNa
RESULT 4 A54985 BMP receptor precursor - African clawed frog C; Species: Xenopus laevis (African clawed frog) C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 31-Dec-2004 C;Arcession: A54988 C;Arcesion: A54988	A; Residues: 1-502 < YAM> A; Residues: 1-502 < YAM> A; Cross-references: UNIPARC: UPI00000E6BDE C; Keywords: ATP; Glycoprotein; transmembrane protein F;127-1498/Domain: transmembrane #status predicted < TMM> F;202-498/Domain: protein kinase homology < KIN> F;210-218/Region: protein kinase ATP-binding motif F;284,343,388/Binding site: carbohydrate (Asn) (covalent) #status predicted
t ventra	Ouery Match 68.2%; Score 1934.5; DB 2; Length 502; Best Local Similarity 72.1%; Pred. No. 1.6e-96; Matches 364; Conservative 60; Mismatches 76; Indels 5; Gaps 5;
not compared	QY 29 MLHGTGMKSDVDQKKPENGVTLAPEDTLPFLKCYCSGHCPDDAINNTCIINGHCFAIIEE 88
	OY 89 DDGGTTLTSGCMKYEGSDFQCKDSPKAQLRRTIECC-RTNLCNQYLQPTLPPVVJGPFF 147
Query Match 78.3%; Score 2223; DB 2; Length 527; Best Local Similarity 80.0%; Pred. No. 6.3e-112; Matches 423; Conservative 44; Mismatches 52; Indels 10; Gaps 5;	QY 148 DGSVRWIAVLISWAVCIVAMIVESSCFCYKHYCKSISSRGRYNRDLEQDEAFIPVGESLK 207
Qy 7 YIRLLGACLFIISHVQQQNLDSMLHQTGMKSDVDQKKPENGYTLAPEDTLPFLKCYCSGH 66 :	QY 208 DLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQVGKGRYGEVWMGKWRGEKVAVKVFFTTE 267 :
Qy 67 CPDDAINNTCITNGHCFAIIEEDDQGETTLTSGCMKYEGSDFQCKDSFKAQLRRTIECCR 126	Qy 268 EASWFRETEIXQTVLARHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDFLKCATLD 327
Qy 127 TWLCNQYLQPTLPPVVIGPFPDGSVRWLAVLISWAVCIVAMIVF-SSCFCYKHYCKSI 183 : : :	Qy 328 TRALLKLAYSAACGLCHLHTEIYGTQGKPAIAHRDLKSKUNLIKKNGSCCIADLGLAVKF 387 ::: : :
QY 184 SSRCRYNRDLEQDEAFIFVGESLKDLIDGSQSGGGGGLFLLVQRTIAKQIQMVRQVGKG 243	QY 388 NSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIWEMARRCITG 447
Cy 244 RYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTGSWT 303 [Qy 448 GIVEEYQLPYXNMVPSDPSYEDMREVVCVKRLRPIVSNRWNSDECLRAVLKLMSECWAHN 507
Oy 304 QLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTGCKPAIAHRDL 363	Qy 508 PASRLTALRIKKTLAKMVESQDVKI 532
364 KSKNILIKKNGSCCIADLGLAVKENSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKNHFQ	RESULT 6 A5344 activin receptor-like kinase 6 precursor - mouse
QY 424 PYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNWVPSDPSYEDMREVVCVKRLRPIV 483	C;Species: Mus musculus (house mouse)

us-10-600-645-2.rpr

receptor for

PIDN prot

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A,Cross-references: UNIPROT:Q05438; UNIPARC:UPI000012643C; GB:D13432; NID:g222862; C;Superfamily: Serine/threonine-specific protein kinase, activin receptor II type; C;Keywords: ATP; phosphotransferase; transmembrane protein F;202-498/Domain: protein kinase homology kIN» F;202-498/Domain: protein kinase ATP-binding motif
           DNA Seq. 3, 297-302, 1993
A/Tille: A new receptor protein kinase from chick embryo related to type II
A/Reference number: A56683; MUID:94003400; PMID:8400359
A/Accession: A56683
A/Actus: preliminary
A/Actus: preliminary
A/Actus: preliminary
A/Actus: preliminary
A/Actus: DA/Actus: DA/Actus: DA/Actus: DA/Actus: DA/Actus: 1-502 <SUM>
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C; Date: 19-Way-1994 #sequence_revision 19-Way-1994 #text_change 05-Oct-2004
C; Accession: A53444; S40159
E; remachita, H.; Ichijo, H.; Franzen, P.; Laiho, M.; Miyazono, K.; Heldin Science 264, 101-104, 1994
A; Title: Characterization of type I receptors for transforming growth factor-beta and ac A; Recession: A53444
A; MuDD: 94188705; PMID: 8140412
A; Accession: A53444
A; Status: preliminary
A; Wolyer mRNA
A; Residues: 1-502 arEN>
A; Cross-reference uniper: A: Orimaby. S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
B; Miyazono, K.; Moren, A.; Grimaby. S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
B; Miyazono, C.; Moren, A.; Grimaby. S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
B; Miyazono, C.; Moren, A.; Grimaby. S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
B; Miyazono, C.; Moren, A.; Grimaby. S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
B; Description: ALK-3 and ALK-6: the closely related members in the serine/threonine kina
A; Recession: S40159
A; Status: preliminary
A; Moleule type: mRNA
A; Residues: 1-502 and ANY
A; Residues: 1-502 and ANY
A; Cross-references: UNIPARC:UPI00000417C; EMBL: Z23143; NID:9437870; PIDN:CAA80674.1; PI
C; Superfamily: Serine/threonine-specific protein kinase, transmembrane protein
F; 202-498/Domain: protein kinase homology and activin kinase; transmembrane protein
F; 202-218/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EASWFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 TRALLKLAYSAACGLCHLHTEIYGTQGKPAIAHRDLKSKNILIKKNGSCCIADLGLAVKF 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLRPIVSNRWNSDECLRAVLKLMSECWAHN 507
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C;Species: Gallus gallus (chicken)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYCKSISSRGRYNRDLEQDEAFIPVGESLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLIDQSQSSGSGSCLPLLVQRTIAKQIQMVRQVGKGRYGEVWMGKWRGEKVAVKVFFTTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 ISDTNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILMEIARRCVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.1%; Score 1933.5; DB 2; Length 502; 72.1%; Pred. No. 1.8e-96; ive 60; Mismatches 76; Indels 5;
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Best Local S
Matches 364
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C;Accession: A56683 R;Sumitomo, S.; Saito, T.; Nohno,

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Crown musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 05-Oct-2004
C;Accession: JC2061
B;Tomoda, T:; Kudoh, T:; Noma, T:; Nakazawa, A.; Muramatsu, M.; Arai, K.
Biochen. Biophys: Res. Commun. 198, 1054-1062, 1994
A;Title: Molecular cloning of a mouse counterpart for human TGF-beta type I receptor.
A;Reference number: JC2061; MUID:94161714; PMID:8117261
A;Accession: JC2061
A;Molecule type: mRNA
A;Residues: 1-503 <TOM>A;Residues: 1-503 <TOM>A;Residues: Teferences: UNIPROT:064729; UNIPARC:UPI0000021038; GB:D28526; NID:9467521; PIDN: C;Comment: This protein is the mouse counterpart for human transforming growth factor be C;Keywords: ATP; glycoprotein; receptor; transmembrane protein
C;Comment: signal sequence #status predicted <SIGS
F;21-501/Product: transforming growth factor-beta type I receptor ESK 2 #status predictef <TWM>F;126-147/Domain: stransmembrane #status predicted <TWM>F;21-501/Product: ransmembrane #status predicted <TWM>F;21-501/Product: Transmembrane #status predicted <TWM>F;21-501/Production F;21-501/Production F
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                                                                                                                                                                                                                                                                                                                       LISGCMKYEGSDFQCKDSPKAQLRRTIECCR-INLCNQYLQPTLPPVVIGPFFDGSVRWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSGSGGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRE
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                                                                                                                                                                                                      SSGSGSCLPLLVQRTIAKQIQMVRQVGKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYSAACGLCHLHTEIYGTQGKPAIAHRDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEV
                                                                                                                                                              36 KSDVDQKKPENGVTLAPEDTLPFLKCYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETT
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                                                                                     Gaps
                                                                                     4 ;
67.9%; Score 1926; DB 2; Length 572.3%; Pred. No. 4.4e-96;
tive 59; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRIKKTLAKMVESQDVKI
                                                                                     360; Conservative
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                       135 SLSVPMLIVASLCFTYKRR-EKLRKQPRLINSMCNSQL----SPLSQLVE--OSSGSGS 186
                                                                                                                                                                                                                                                                                                                                                                187 GLPLLVQRTIAKQIQMVRLVGKGRYGEVWLAKWRDERVAVKTFFTTEEASWFRETEIYQT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 VLMRHDNILGFIAADIKGNGSWTQMLLITDYHEMGSLHDYLSMSVINPQKLQLLAFSLAS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 GLAHLHDEIFGTPGKPAIAHRDIKSKNILVKRNGQCAIADFGLAVKYNSELDVIHIAQNP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 VLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 RVGTRRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIWEMARRCIT-----GGIVEEYQ 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPYYNMVPSDPSYEDMREVVCVKRLRPIVSNRWNSDECLRAVLKLMSECWAHNPASRLTN 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 NSMCIAEIDLIPRDRPFVCAPSSKTGAVTTTYCCNQDHCNKIELPTTEKQSAGLGPVELA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204
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      LTCYCDGSCPDNVSNGTCETRPGGSCFSAVQQLYDETTGMYEEERTYGCMPPEDNGGFLM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transforming growth factor beta receptor type I precursor - mouse C; Species: Mus musculus (house mouse) C; Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVCIVAMIVESSCFCYKHYCKSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 GLCHLHTEIYGTQGKPAIAHRDLKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 KKPENGVILAPEDIL----PFLKCYCSGH-CPDDAINNTCIINGHCFAIIEEDDQGETTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYCKSISSRGRYNRDLEQDEAFIPVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
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                                                                   CKDSPKAQLR-RIIECC-RINLCNQYLQPILPPVVIGPFD----
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6.3e-61;
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51.4%; Pred. No. 6.3e.
:ive 70; Mismatches
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51; Conservative
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LRVKKTLGRL 496
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C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Stecession-rat-1996 #sequence_revision 09-Mar-1996 #text_change 05-Oct-2004
C; Stecession-rat-1994
R; Brummel, T.J.; Twombly, V.; Marques, G.; Wrana, J.L.; Newfeld, S.J.; Attisano, L.; Mas
Cell 78, 251-251, 1994
A; Title: Characterization and relationship of Dpp receptors encoded by the saxophone and A; Reference number: A54829; MUID:94320137; PMID:8044839
A; Ritle: Characterization and relationship of Dpp receptors encoded by the saxophone and A; Reference number: A54829; MUID:94320137; PMID:8044839
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-509 <RES>
A; Crosserieferences: FBJRase: FBBJRA003716
C; Genetics:
A; Crosserieferences: FBJRase: FBBJRA003716
C; Genetics:
A; Crosserieferences: FBJRase: FBBJRA003716
C; Genetics:
B; 198-500/Domain: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLRPIVSNRWNSDECLRAVLKLMSEC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSIGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAXIMREC 474
                                                                                                                                                                                                                                                     KKPENGVTLAPEDTL----PFLKCYCSGH-CPDDAINNTCITNGHCFAIIEEDDQGETTL
                                                                                                                                                                                                                                                                                                                 RRPQLLIVLVAAATLLPGAKALQCFC--HLCTKD--NFTCETDGLCFVSVTETTD-KVIH
                                                                                                                                                                                                                                                                                                                                                                                    TSGCMKY----EGSDFQCKDSPKAQLRRTIECCRINLCNQYLQPTLPPVVIGPFFD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSMCIAEIDLIPRDRPFVCAPSSKTGAVTTTYCCNQDHCNKIELPT----TGPFSEKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GSVRWLAVLISMA--VCIVAMIVFSSCFCYKHYCKSISSRGRYNRDLEQDEAFIPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 FTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDFLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 YTVTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQVGKGRYGEVWMGKWRGEKVAVKVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 ATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAHRDLKSKNILIKKNGSCCIADLGL
                                                                                                                                                                                           32;
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                                                            F;41/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                  Length 503;
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                                                                                                                     Query Match 44.9%; Score 1274; DB 2; Length 5 Best Local Similarity 51.7%; Pred. No. 3.1e-61; Matches 263; Conservative 70; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 44.9%; Score 1274; DB 2; Length 5 il Similarity 53.5%; Pred. No. 3.1e-61; 262; Conservative 63; Mismatches 133; Indels
F;203-499/Domain: protein kinase homology «KIN» F;211-219/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WAHNPASRLTALRIKKTLAKMVESQDVKI 532
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                                                                                                                                                                                                                      HMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATDTIDIAPNHRVGTK 376
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Nichernate names: TGFbeta type I receptor ALK-5
Nicontains: protein Kinase (EC 2.7.1.37)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 SPKAQLRRTIECCRTNLCNQYLQPT-----LPPVVIGPFFDGSVRWLAVLISMAVCIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 ITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLRPIVSNRWNSDECLRAVLKLMSECW
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44.7%; Score 1268; DB 2;
Best Local Similarity 52.8%; Pred. No. 6.4e-61;
Matches 257; Conservative 67; Mismatches 133;
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A; Residues: 1-509 < MAT>
A; Centerces: UNIPROT: 004771; UNIPARC: UDI00000163F; CB: L02911; NID: 9338218; PIDN: R; ten Dijke, P.; Ichijo, H.; Franzen, P.; Schulz, P.; Saras, J.; Toyoshima, H.; Heldin, Oncogene 8, 2879-2887, 1993
A; There are ceptor-like kinases: a novel subclass of cell-surface receptors with A; Reference number: 137161; MUID: 93390967; PMID: 8397373
A; Reference number: 137162
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Mesidues: 1-509 < RES>
A; Gestidues: 1-509 < RES>
A; Gestidues: 1-509 < RES>
A; Cross-references: UNIPARC: UPI000000163F; EMBL: Z22534; NID: 9402184; PIDN: CAA80256.1; PI
C; Genetics:
A; Gene: GDB: ACVR1; ACVRIK2; SKR1; ALK2
A; Cross-references: GDB: 216986; OMIM: 601298
C; Reywords: ATP; serine/threonine-specific protein kinase; transmembrane protein F; 206-502/Domain: protein kinase ATP-binding motif
                        kir
                                                                                                                                    act
activin A receptor type I - human
NyAlternate names: activin A receptor type II-like kinase 2; ALK-2; serine/threonine I
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Dec-2004
C;Datesosion: A45992; I37162; S37182
R;Matsuzaki, K.; Xu, J.; Wang, F.; McKeehan, W.L.; Krummen, L.; Kan, M.
J. Biol. Chem. 268, 12719-12723, 1993
A;Title: A widely expressed transmembrane serine/threonine kinase that does not bind A;Reference number: A45992; MUID:93286114; PMID:8389764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.4%; Score 1204.5; DB 2;
48.6%; Pred. No. 1.6e-57;
Live 79; Mismatches 132;
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Best Local Similarity
Matches 253; Conserv
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14

RESULT A55921

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serine/threonine kinase Atr-1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 31-Dec-2004
C;Accession: A55921
R;Wrana, J.L.; Tran, H.; Attisano, L.; Arora, K.; Childs, S.R.; Massague, J.; O'Connor, Mol. Cell. Biol. 14, 944-950, 1994
A;Title: Two distinct transmembrane serine/threonine kinases from Drosophila melanogast A;Reference number: A55921
A;Reference number: A55921; MUID:94119112; PMID:8289834
A;Accession: A55921
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-601 <WRA>
A;Residues: 1-601 <WRA>
A;Coss-references: UNIPROT:Q23975; UNIPARC:UPI00007A851; GB:U04692; NID:g436960; PIDN C;Gene: FlyBase:babo
C;Gene: FlyBase:babo
A;Cross-references: RlyBase:FBgn0011300
C;KGywords: AFP
F;301-597/Domain: protein kinase homology <KIN>
F;303-317/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 0.2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C;Accession: A49664 w.W.
R;Tsuchida, K.K.T.; Vale, W.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11242-11246, 1993
A;Title: Cloning and characterization of a transmembrane serine kinase that acts a A;Reference number: A49664; MUID:94068580; PMID:8248234
A;Reference number: A49664; MUID:94068580; PMID:B20BU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 YLTTHPVDTNTMLNMSLSIATGLAHLHMDIVGTRGKPAIAHRDLKSKNILVKSNLSCAIG
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42.2%; Score 1198; DB 2; Length 60
Best Local Similarity 46.3%; Pred. No. 4.1e-57;
Matches 237; Conservative 83; Mismatches 138; Indels
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MKECWYPNPVARLTALRIKKTLASISVEDKVK 600
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us-10-600-645-2.rpr

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A;Molecule type: mRNA
A;Residues: 1-509 <RES>
A;Residues: 1-509 <RES>
Cross-references: UNIPROT:P80201; UNIPARC:UP10000126671; GB:L19341; NID:g435431; PIDN:G;Keywords: ATP
F;206-502/Domain: protein kinase homology <KIN>
F;214-222/Region: protein kinase ATP-binding motif
                                                                                                                                    12;
                                                                                                                                                                                                                                                                            61 CYCSG-----HCPDDAINNTCITNGHCFAIIEEDDQGETTLTSGCMK-YEGSDFQCKD 112
                                                                                                                                                                                                                     113 SPKAQLRRTIECCRTNLCNQYLQPTLPPVVIGPFFDGS-----VRWLAVLISMAVCIVA 166
                                                                                                                                                                                                                                          84 PPSP--GQAVECCQGDWCNRNVTARLP--TKGKSFPGSQNFHLEVGLIILSVVFAVCLFA 139
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                                                                                                      Length 509;
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Best Local Similarity 50.5%; Pred. No. 5.8e-57;
Matches 247; Conservative 75; Mismatches 127;
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Search completed: December 3, 2005, 06:12:27 Job time: 42 secs

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1 MTQLYTYIRLLGACLFIISH......TALRIKKTLAKMVESQDVKI
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        Bus scrofa

        36
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
                                                                                                                                                                     Gaps
Pfam; PF01064; Activin_recp; 1.
PRINTS; PR00653; PKinase; 1.
PRINTS; PR00653; ACTIVINZR.
SMART; SM00467; GS; 1.
PROSITE; PS00107; PROTEIN_KINASE ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nucleotide-Dinding; Receptor;
Serine/threonine-protein kinase; Signal; Transferase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=95204990; PubMed=7897267;
Takeda K.;
"Expression of serine/threonine kinase receptors during ectopic bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI 532
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                                                                                                                                                                    Indels
                                                                                                                        14ED4C03E2540A0C CRC64;
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                             Ouery Match
100.0%; Score 2838; DB 2;
Best Local Similarity 100.0%; Pred. No. 9.3e-188;
Matches 532; Conservative 0; Mismatches 0;
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                                                                                                                      532 AA; 59994 MW;
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Q78EA7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .; IEA.
formation induced by bone morphogenetic protein (BMP).";

Kokubyo Gakkai Zasshi 61:512-526(1994).

-!- CATALYTIC ACTIVITY: ATP + a protein (BMP).";

-!- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).

-!- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).

EMBL: 975393; AAB33865.1; -; mRNA.

REMBL: 975895; Bampria.

RESP: 70889; Bmpria.

RGD: 60:0004713; Fart binding; IEA.

RGD: G0:0004713; Fart binding; IEA.

RGD: G0:0004713; Froceptor activity; IEA.

RGD: G0:0004872; Freceptor activity; IEA.

RGD: G0:0004872; Freceptor activity; IEA.

RGD: G0:0004872; Freceptor activity; IEA.

RGD: G0:000524; Fitransforming growth factor beta receptor ac. .; II

RGD: G0:0007178; Pitransforming growth factor beta receptor ac. .; II

RGD: G0:0007178; Pitransforming growth factor beta receptor ac. .; II

RGD: G0:0007178; Pitransforming acid phosphorylation; IEA.

RGD: G0:0007178; Pitransforming scout in serine/threo. .; II

REPPO: IPRO00733; Activin receptor

InterPro: IPR00333; Actn. receptorII.

InterPro: IPR00371; Ser_thr_pkinase.

InterPro: IPR00465; TGFBetarecept GS.

InterPro: IPR00465; TGFBetarecept GS.

InterPro: IPR00465; TGFBetarecept GS.

InterPro: IPR00465; Pitransforming FR00665.

REMBL: PF00665; Rinase: II.

REMBL: PF00665; Rinase: II.

REMBL: PF00665; Rinase: II.

REMBL: PF00665; Rinase: II.
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PRODOM; PROMOGS; ACTIVINZR.
PRODOM; PROMOGS; ACTIVINZR.
PRODOM; PROMOGS; STKC; 1.
SWART; SMO0220; STKC; 1.
PROSITE; PSO0109; TYKC; 1.
PROSITE; PSO0109; PROTEIN_KINASE_DOM; 1.
PROSITE; PSO0108; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Nocleoitde-Ending; Receptor; SCRINC/Chreonine-Protein &inase; Transferase; Transmembrane.
SCRINC/Chreonine-Protein &inase; Transferase; Transmembrane.
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Pred. No. 9.3e-188;
; Mismatches 0;
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100.0%; Sc
Best Local Similarity 100.0%; Pr
Matches 532; Conservative 0;
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A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B.S., Wagner L., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibe F.,
A Altschul S.F., Zeeberg B. Buelove K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Bonaldo M.F., Carninci P., Scheetz T.E.,
B Connetein M.J., Usdin T.B., Toodhyuki S., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Toodhyuki S., Carninci P., Frange C.,
A Richards S., Morley K.C., Hale S., Garca A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield M., Schein J.E., Jones S.J.M., Marra M.A.;
C. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUCLEOTIDE SEQUENCE.
MEDLINE=94344106; PubMed=8065329;
Koenig B.B., Cook J.S., Wolsing D.H., Ting J., Tiesman J.P.,
Correa P.E., Olson C.A., Pecque A.L., Ventura F., Grant R.A.,
Chen G., Wrana J.L., Massague J., Rosenbaum J.S.;
"Characterization and cloning of a receptor for BMP-2 and BMP-4 from
                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Bone morphogenetic protein receptor type IA precursor (EC 2.7.1.37)
(Serine/threonine-protein kinase receptor R5) (SKRS) (Activin receptor-like kinase a) (ALK-3) (BMP-2/BMP-4 receptor)
Mame=Bmprla; Synonyms=Acvrlk3, Bmpr;
Mus musculus (Mouse)
                             532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95024092; PubMed=7937936;
Suzuki A., Thies R.S., Yamaji N., Song J.J., Wozney J., Murakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A truncated bone morphogenetic protein receptor affects dorsalventral patterning in the early Xenopus embryo.";
Proc. Natl. Acad. Sci. U.S.A. 91:10255-10259(1994).
                                                                                                                                                                                                                                                                                                                                     STRAIN=Swiss; TISSUE-Embryo; MEDLINE=95269711; PubMed=7750489; DOI=10.1210/en.136.6.2652; MEDLINE=95269711; PubMed=7750489; DOI=10.1210/en.136.6.2652; Dewulf N., Verschueren K., Lonnoyo O., Moren A., Crimsby S., Spiegle K., Miyazono K., Huylebroeck D., ten Dijke P.; "Distinct spatial and temporal expression patterns of two type receptors for bone morphogenetic proteins during mouse
             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH 3T3 cells.";
Mol. Cell. Biol. 14:5961-5974(1994).
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                                                                                                    STANDARD;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
SUBUNIT: Heterodimer with a type-II receptor.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUB SPECIFICITY: Widely expressed.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. TGPB receptor subfamily.
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ATP (By similarity).
N-linked (GlcNAc. . .) (Potential)
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Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
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Matches 526; Conservative
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532 AA;
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[1] —
NUCLEOTIDE SEQUENCE.
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                                             121 TIECCRINLCNQYLQPTLPPVVIGPFFDGSIRWLVVLISMAVCIVAMIIFSSCFCYKHYC 180
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CYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
                            121 TIECCRTNLCNQYLQPTLPPVVIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYC 180
                                                                                                                                                                                                              SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTOGKPAIAH 360
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AN INCLECTIVE SEQUENCE.

A Shalamanov P.D., Morty R.E., Eickelberg O.;

STAIN-BALB/C; TISSUE-Lung;

Shalamanov P.D., Morty R.E., Eickelberg O.;

Shalamanov P.D., Morty R.E., Eickelberg O.;

T. Expression of bone morphogenic protein receptor la in the mouse.";

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

C. --- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

C. --- SIMILARITY Belongs to the Ser/Thr protein kinase family.

DR SMR; OS1343; S5-143.

DR GO; GO:0005615; C:axtracellular space; TAS.

GO; GO:0005615; C:axtracellular space; TAS.

BR GO; GO:0005615; C:axtracellular space; TAS.

GO; GO:0005615; C:axtracellular space; IAS.

GO; GO:0009516; P:cartiage development; IMP.

GO; GO:00015216; P:cartiage development; IMP.

GO; GO:0001989; P:ectoderm development; IMP.

GO; GO:0001980; P:mesendoderm development; IMP.

DR GO; GO:0001980; P:meleriar development; IMP.

GO; GO:0001980; P:meleriar development; IMP.

GO; GO:0001980; P:meleriar development; IMP.

BR InterPro; IPR000313; Activin, receptor!

BR InterPro; IPR000139; Proc*kinase.

DR InterPro; IPR000199; Ser_thr_pkin AS.

BR InterPro; IPR000190505; Tath. pkin AS.

DR InterPro; IPR000190505; Tath. pkin AS.

DR InterPro; IPR0001946; Tath. pkin AS.

DR InterPro; IPR0001946; Tath. pkin AS.

DR InterPro; IPR00019605; Tath. pkin AS.

DR InterPro; IPR00019606; Tath. pkin AS.

DR InterPro; IPR00019606; Tath. pkin AS.

DR InterPro; IPR00019606; Tath. pkin AS.
                                                                                                                                                                   241 GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG
                                                                                                         KSISSRGRYNRDLEQDEAFI PVGESLKDLI DQSQSSGSGGLPLLVQRTIAKQI QMVRQV
                                                                                                                                                  GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG
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                                                                                        KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Bone morphogenetic protein receptor type 1a.
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13 MOUSE
Q53Z43 MOUSE PRELIMINARY;
Q53Z43;
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NUCLEOTIDE SEQUENCE.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTQLYTYIRLGACLFIISHVQGQNLDSMLHGTGMKSDLDQKKPENGVTLAPEDTLPFLK
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01-UN-1994 (Rel. 29, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Bone morphogenetic protein receptor type IA precursor (EC 2.7.1.37)
(Serine/threonine-protein kinase receptor RS) (SKRS) (Activin receptor-like kinase 1) (ALK-3).
Homo sapieng (Human)
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SEQUENCE 532 AA; 60063 MW; 70CC83CFB07CE9D5 CRC64;
               Prints, Prodes, Prinase, 1.
PRINTS, PRO065; Prinase, 1.
PRINTS, PRO0653; ACTIVINZR.
SWART; SM00467; 62; 1.
SWART; SM00220; STKC; 1.
SWART; SM00219; TYrKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOW; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nuclectide-binding; Receptor;
                                                                                                                                                                                                                                                                                                                                                    99.5%; Score 2823; DB 2; 98.9%; Pred. No. 1e-186; iive 5; Mismatches 1
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Matches 526; Conservative
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MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altasner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hashe F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Multing M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
M. Marian M.A., Schein J.E., Jones S.J.M., Marra M.A.,
Scherztion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21426344; PubMed=11536076; Zhou X.-P., Woodford-Richens K., Lehtonen R., Kurose K., Aldred M., Lahou X.-P., Woodford-Richens K., Lehtonen R., Karose K., Aldred M., Hampel H., Launonen V., Virta S., Pitarski R., Salovaara R., Jaervinen W.F., Conrad B.A., Dunlop M., Hodgson S.V., Iwama T., Jaervinen H., Kellokumpu I., Kim J.C., Leggett B., Markie D., Mecklin J.-P., Neale K., Phillips R., Piris J., Rozen P., Houlston R.S., Aaltonen L.A., Tomlinson I.P.M., Eng C.; "Germline mutations in BMPRIA/ALM2 cause a subset of cases of juvenile polyposis syndrome and of Cowden and Bannayan-Riley-Ruvalcaba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 55-143 IN COMPLEX WITH BMP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sayed M.G., Almed A.F., Ringold J.R., Anderson M.E., Bair J.L., Mitros F.A., Lynch H.T., Tinley S.T., Petersen G.M., Giardiello F.M., Vogelstein B., Howe J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21275975; PubMed=11381269; DOI=10.1038/88919; Howe J.R., Bair J.L., Sayed M.G., Anderson M.E., Mitros F.A., Pettersen G.M., Velculescu V.E., Traverso G., Vogelatein B.; "Germline mutations of the gene encoding bone morphogenetic protein receptor 1A in juvenile polyposis.";
                      MEDLINE=931390967; PubMed=81397373; ten Dijke P., Ichijo H., Franzen P., Schulz P., Saras J., Toyoshima H., Heldin C.-H., Miyazono K.; "Activin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine kinase activity."; Oncogene 8:2879-2887(1993).
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PubMed=12136244; DOI=10.1007/s00439-002-0748-9;
Friedl W., Uhlhaas S., Schulmann K., Stolte M., Loff S., Ba Mangold E., Sterrn M., Knaebel H.P., Sutter C., Weber R.G., Pistorius S., Burger B., Propping P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10891198; DOI=10.1038/75903;
Kirsch T., Sebald W., Dreyer M.K.;
"Crystal structure of the BMP-2-BRIA ectodomain complex.";
Nat. Struct. Biol. 7:492-496(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS JPS ARG-124 AND TYR-376, AND VARIANT CD ASP-338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Am. J. Hum. Genet. 69:704-711(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA sequences."
TISSUE=Placenta;
MEDLINE=93390967;
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Note that the state of the stat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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SWART; SMO0210; STKC; 1.
SWART; SMO0219; TYKC; 1.
SWART; SMO0219; TYTKC; 1.
SWART; SMO0219; TYTKC; 1.
PROSITE; PSO1010; PROTEIN KINASE ATP; 1.
PROSITE; PSO1018; PROTEIN KINASE DOM; 1.
PROSITE; PSO1018; PROTEIN KINASE ST; 1.
Nucleotide-binding; Receptor; Serine/threonine-protein; Kinase; Signal; Iransmembrane.
I 23 Potential.
  common in MADE 4
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GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0007179; P:transforming growth factor beta receptor si. .

InterPro; IPR000472; Actur receptor.

InterPro; IPR000313; Actur receptorII.

InterPro; IPR000821; Ser thr pkin AS.

InterPro; IPR000821; Ser thr pkin ase.

InterPro; IPR0002290; Ser thr pkin ase.

InterPro; IPR001245; TGPBetarecept_GS.

InterPro; IPR001245; Tyr pkin ase.

Pfam; PF01064; Actifur recp; 1.
                       mutation carriers than in BMPRIA mutation carriers.";
Hum. Genet. 111:108-111(2002).
"Juvenile polyposis: massive gastric polyposis is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1ES7; X-ray; B/D=55-143.
PDB; 1REW; X-ray; C/D=24-152.
Ensembl; ENSG0000107779; Homo sapiens.
HGNC; HGNC:1076; BMERIA.
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PIR; 137163; 137163.
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                                                                                                VARIANT JPS THR-470
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421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
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                                                                                                                                           Name-Empria;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
MEDLINE=94344106; PubMed=8065329;
Koenig B.B., Cook J.S., Wolsing D.H., Ting J., Tiesman J.P.,
Correa P.E., Olson C.A., Pecquet A.L., Ventura F., Grant R.A.,
Chen G., Wrana J.L., Massague J., Rosenbaum J.S.;
"Characterization and cloning of a receptor for BMP-2 and BMP-4 from
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                    PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI
                              PI VSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI
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                                                                                                      Created)
Last sequence update)
Last annotation update)
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PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-Dinding; Kinase; Nucleotide-Dinding;
                                                                                      PRT;
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(TrEMBLrel. 01, 1
(TrEMBLrel. 26, 1
                                                                                    QE0607 MOUSE PRELIMINARY;
Q60607;
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01-NOV-1996
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 3one morphogenetic protein receptor type
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                                    Cytoplasmic (Potential).
Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
N-linked (GlcNAc. . .) (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                Length 532;
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                   Extracellular (Potential)
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Pred. No. 1.4e-182;
7; Mismatches 9;
                                                                                                                                                                                                                                                                     /FTId=VAR 022831.

M -> T (in JPS).

/FTId=VAR 022832.

P -> T (in Ref. 1).
                                                                                                                                                                                                                             /FIId=VAR_015534.
C -> Y (in JPS).
/FTId=VAR_015535.
R -> C (in JPS).
                                                                                                                                            Y -> D (in JPS).
/FTId=VAR_022828.
C -> Y (in JPS).
/FTId=VAR_022829.
                                                                                                                                                                       /FTId=VAR 022829.
C -> R (in JPS).
/FTId=VAR 015533.
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/FTId=VAR 022830.
A -> D (in CD).
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llarity 97.0%;
Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                    KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV
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Last annotation update)
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PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-Dinding; Kinase; Nucleotide-Dinding;
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ProDom; PD000001; Prot_kinase; 1.
SMART; SM00467; GS; 1.
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                                                 61 CYCSGHCPDDAINNTCITNGHCFAIIEEDEHGEPTLASGCMKYEGSDFQCKDSPKAQLRR 120
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                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE.
MEDLINE=20237589; PubMed=10772803; DOI=10.1006/dbio.2000.9684;
MEDLINE=20237589; PubMed=10772803; DOI=10.1006/dbio.2000.9684;
MCPherson C.E., Varley J.E., Maxwell G.D.;
"Expression and regulation of type I BMP receptors during early avian sympathetic ganglion development.";
Dev. Biol. 221:220-232(2000).
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein kinase family.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HRDLKSKNILLIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSK
                                                                                                                                                                                          1 MTQLYTYIRLLGACLFIISHVQGQNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                         Gape
                                                                                                                                      1;
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                                                                                      533;
Serine/threonine-protein kinase; Transferase; Transmembrane. SEQUENCE 533 AA; 60283 MW; C39C8267DB494DBE CRC64;
                                                                                      Length
                                                                                                                                         Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                             ; Score 2582.5; DB 2;
; Pred. No. 4.3e-170;
22; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 AA
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SMR; Q9PUF5; 55-139.

G0; G0:0016020; C:membrane; IEA.

G0; G0:0005524; F:meceptor activity; IEA.

G0; G0:0004872; F:receptor activity; IEA.
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                                                                                   91.0%;
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Q9PUFS;
                                                                                                                                         Matches 481; Conservative
                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TIECCRINLCNQYLQPTLPPV-VIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHY 179
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Stanopus laevis (African Clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
GO; GO:0005024; F:transforming growth factor beta receptor ac. GO; GO:0006468; P:protein amino acid phosphorylation; IEA. GO; GO:0007178; P:transmembrane receptor protein serine/threo. InterPro; IPR000472; Activin_receptor].
InterPro; IPR000333; Activin_receptor].
InterPro; IPR000313; Activin_receptor].
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR003571; Ser_thr_pkin_AS.
Pfam; PF01064; Activin_recp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 533;
                                                                                                                                                                                                                                                                                                                                              Serine/threonine-protein kinase; Transferase; Transmembrane.
SEQUENCE 533 AA; 60243 MW; 40519BB4034COCCF CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                 PRINTS; PROOGS3; ACTIVINZR.
ProDom; PD000001; Prot_kinase; 1.
Prodom; SM0467; GS; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
ATP-binding; Kinase; Nuclectide-binding; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                                                                                                                                                                                                                                                                                                                           90.6%; Score 2570.5; DB 2, 89.7%; Pred. No. 2.9e-169; iive 23; Mismatches 31;
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Matches 478; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         GO, GO:0016020; C:nembrane; IEA.
GO; GO:0016020; C:nembrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000524; F:recanaforming growth factor beta receptor ac. .; IEA.
GO; GO:0005468; P:protein amino acid phosphorylation; IEA.
GO; GO:0007178; P:transmembrane receptor protein serine/threo. .; IEA.
InterPro; IPR000472; Activin_receptor.
InterPro; IPR000472; Activin_receptor.
InterPro; IPR00019; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin AS.
InterPro; IPR03565; TGFDetarecept_GS.
Pfam; PF01064; Activin_recp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 YIRLLGACLFIISHVQGQNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLKCYCSGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIACFGALLLVI-HTQGQDFNILPHRTGMKSNSDPKKQENGVTLAPEDTLPFLNCYCSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
WUCLEOTIDE SEQUENCE.
MEDLINE=5500777; PubMed=7522972; DOI=10.1016/0092-8674(94)90409-X; Graff J., Melton D.;
Graff J., Melton D.;
Studies with a Xenopus BMP receptor suggest that ventral mesodermiducing signals override signals in vivo.";
Cell 79:169-179(1994).
-! SUBCELULAR LOCATION: Type I membrane protein (By similarity).
-! SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; U16654; AAAS8707.1; -; mRNA.
HSSP; R56894; LESY.
SMR; Q91578; 53-140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 2223; DB 2; Length 527;
; Pred. No. 2.9e-145;
44; Mismatches 52; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00107; PROTEIN_KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclectide-binding; Receptor;
Serine/threonine-protein kinase; Transferase; Transmembrane.
SEQUENCE 527 AA; 59800 MW; 53AFB5BEE046512B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00653; ACTIVINZR.
ProDom; PD000001; Prot_kinase; 1.
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.;
A Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
A Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;
A placthench L.; Marusina K.F.; Farmer A.A.; Rubin G.M.; Hong L.;
A stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
A brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
A Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;
A Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Guaratne P.H.;
A Richards S., Worley K.C.; Hale S., Garcia A.M.; Gay L.J.; Hulyk S.W.;
A Nilalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
A Rahay J.; Helton E.; Ketteman M.; Madan A.; Rodrigues S.; Sanchez A.;
Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
A Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
Butterfield Y.S.M.; Krzywinski M.I.; Skalska U.; Smailus D.E.;
Butterfield Y.S.M.; Krzywinski M.I.; Skalska U.; Smailus D.E.;
A polentation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suzuki A., Shioda N., Ueno N.; "Bone morphogenetic protein acts as a ventral mesoderm modifier in
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                        527
             SNRWNSDECLRAVLKLMAECWAQNPASRLTALRIKKTLAKMVESQDVKI
SNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                  527
                                                                                                                                                                                                                                                                         / Xenopus embryos.";
Growth Differ. 37:581-588(1995).
                                                                                  PRT;
                                                                                                         Created)
                                                                                                                                                                Xenopus laevis (African clawed frog)
                                                                                                                                         BMP receptor (LOC397711 protein).
Name=LOC397711;
                                                                                                       01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dev. Dyn. 225:384-391 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA sequences."
                                                                                042338_XENLA PRELIMINARY;
                                                                                                     01-JAN-1998 (TrEMBLrel.
                                                                                                                                                                                                                           [1] -
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                 [2]
NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                NCBI_TaxID=8355;
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 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTGSWT 303
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                                          IEA
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Name=LOC397712;
Xenopus laevis (African clawed frog).
Kusryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
R GO; GO:000178; P:transmembrane receptor protein serine/threo. InterPro; IPR000472; Activin_receptor.
R InterPro; IPR000313; Actin_receptor.
R InterPro; IPR000313; Actin_receptor.
R InterPro; IPR000619; Prot_kinase.
R InterPro; IPR0006871; Ser_Lhr_gkin_AS.
R InterPro; IPR0006871; GFE tarrecept_GS.
R Pfam; PF00069; Activin_recp; 1.
R Pfam; PF00069; Rinase; 1.
R Probom; PR000601; Prot_kinase; 1.
R Probom; PR000001; Prot_kinase; 1.
R PROSTTE; PS00117; PROTEIN KINASE ATP; 1.
R PROSTTE; PS00117; PROTEIN KINASE BT; 1.
R PROSTTE; PS00118; PROTEIN KINASE ST; 1.
W ATP-binding; Kinase; Nuclectide-binding; Receptor; Serine/threonine-protein kinase; Transmembrane.
SEQUENCE 527 AA; 59786 WW; BDAECE9DA566B408 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
        GO:0006468; P:protein amino acid phosphorylation; IEA. GO:0007178; P:transmembrane receptor protein serine/threo.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.3%; Score 2222; DB 2;
80.0%; Pred. No. 3.5e-145;
iive 43; Mismatches 53;
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0423397
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R GO; GO:0016220; C:membrane; IEA.

R GO; GO:0016224; F:ATP binding; IEA.

R GO; GO:0004872; F:ATP binding; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0007178; P:transmembrane receptor protein serine/threo. .; IEA.

R InterPro; IPR000313; Actr receptorII.

R InterPro; IPR000313; Actr receptorII.

R InterPro; IPR000371; Ser thr pkin AS.

R InterPro; IPR00871; Ser thr pkin AS.

R InterPro; IPR03605; TGPEtaTeCept_GS.

R Pfam; PF01064; Activin recept_GS.
                                                                                                                                                                                                                                Attausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moorer T., Mans S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Malakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Schlake U., Smallus D.E., Schnerch A. Schimvood J., Schmutz J., Myers R.W., Smallus D.E., Schnerch A., Schnerch A., Schnerch A., Schimson J.W., Stalska U., Smallus D.E., Schnerch A., Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Generation and initial analysis of more than 15,000 full-length human
                                                            Suzuki A., Shioda N., Ueno N.;
Bone mcriphogenetic protein acts as a ventral mesoderm modifier in early Kenopus embryos...
Dev. Growth Differ. 37:581-588(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S., Strausberg R.; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. SUBCELLULAR LOCATION: Type I membrane protein (By similarity). SIMILARITY: Belongs to the Ser/Thr protein kinase family. EMBL; D32067; BAA22438.1; -; mRNA. EMBL; BC071081; AAH71081.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
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                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Vuclectide-binding; Receptor;
Serine/threonine-protein kinase; Transferase; Transmembrane.
SEQUENCE 527 AA; 59807 MW; D24E46D8A1291074 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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ProDom; PD000001; Prot_kinase; 1.
SMART; SM00467; GS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dev. Dyn. 225:384-391(2002).
                                          NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Ovary;
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                                                                                                                                                                  HCPDDAINNTCITNGHCFAIIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRRTIECC 125
                                                                                                                                                                                       64 YCPQNAVNNTCITWGQCFAMIEEDDHGDIIWTSGCMKMEGSDFQCKDSPKALSRRTIECC 123
                                                                                                                                                                                                                                                                                                                                    242
                                                                                                                                                                                                                                                                                                                                                       238 GRYGEVWMGKWRGEKVAVKVFFTAEEASWFRETEIYQTVLMRHENILGFVAADIKGTGSW 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPYIMADIYSFGLIIWEMARRCIIGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLRPI 482
                                                                                                                                                                                                                                                   RINLCNQYLQPTLPPVVIGPFFDG--SVRWLAVLISMAVCIVAMIVF-SSCFCYKHYCKS 182
                                                                                                                                                                                                                                                                          GRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTGSW 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAHRD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOWYLITEYHENGSLYDFLKCTTLDTRSLLKLAYSAACGLCHLHTEIYGTOGKPAIAHRD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 LKSKNILIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKNHF 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                         63
                                                                                   RLLGAC----LFIISHVQGQNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLKCYCSG
                                                                                                                         4 RLFIACFGVLLLAIHAQGQDFNILPHRTGMKSNSDPKKQENGVTLAPEDTLPFLNCYCSG
                                                                                                                                                                                                                                                                                                                                  183 ISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQVGK
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 VSNRWNSDECLRAILKLMAECWAQNPASRLTALRIKKTLAKMVESQDVKI 527
      Length 527;
  77.9%; Score 2211; DB 2; Length 52' 79.4%; Pred. No. 2e-144; ive 42; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Type I serin/threonine kinase receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=bmprla, Synonyms=BMPR-IA;
Brachydanio rerio (Zebrafish) (Danio rerio).
Query Match
Best Local Similarity 79.4'
Matches 421; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O93243 BRARE PRELIMINARY;
093243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is perliahmary date and cc - p-Finorinory pass a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of MPF (By similarity).

CC - SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature occytes (By similarity).

CC -: SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature occytes (By similarity).

CC -: SUBUNIT: Porms a stable but non-covalent complex with cyclin B in mature occytes (By similarity).

CC -: SUBUNIT: Porms a stable but non-covalent complex with cyclin B in mature occytes (By similarity).

CC -: SUBUNIT: Porms a stable but non-covalent complex with cyclin B in mature occytes (By similarity).

CC -: SUBUNIT: Porms a stable but non-covalent complex with cyclin B in mature occytes (By similarity).

CC -: SUBUNIT: Porms a stable but non-covalent complex with cyclin B in mature occytes (By similarity).

CC -: SUBUNIT: Porms of the Ser/Thr protein kinase family.

EMBL: CABCOLOGO STATE PROTEIN KINASE ATP; 1.

CC -: SUBCELLUAR LOCATION; PROTEIN KINASE ATP; 1.

CC -: SUBCELLUAR LOCATI
                                                                                                                Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Manuell S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirco J., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Mincker P., Lander B., Weissenbach J., Roest Crollius H.; Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 -IGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYCKSISSRGRY---NRDLEQDEA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 PIG----GSPNWLAFLISMTVC-CCMLICVAVVCYYRY-KWQSERQRYHKDHRDLEQ-EV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 GONLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLKCYCSGHCPDDAINNTCITNGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GQNPDYVLQGTGVKAE-----DSTIAPEDAARFLSCYCSGHCPEDATNNTCQTNGQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAIIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRRTIECCRTNLCNQYLQPTLPPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE. Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similaricy
nes 403; Conservative
                                                      [1]
NUCLEOTIDE SEQUENCE.
       NCBI_TaxID=99883;
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               NOT THE STANTANT OF THE STANTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECCRTNLCNQYLQPTLPPVVIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYCKS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRYGEVMMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTGSW 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LYTYIRLLGACLFI-ISHVQGQNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPFLKCY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 ISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKQIQMVRQVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 TQLYLITDYHENGSLYDYLKFTTLDTQALLRLAFSAACGLCHLHTEIYGTQGKPAIAHRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF15083, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                    PRINTS; PRO065; ATTUTINE.
PRODOM; PRO0601, Prot_kinase; 1.
SMART; SMO467; GS; 1.
PROSTTE; PSO1010; PROTEIN_KINASE ATP; 1.
PROSITE; PSO1010; PROTEIN_KINASE_DOM; 1.
PROSITE; PSO10109; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nucleotide-binding; Receptor;
SETINE/Khreonine-protein kinase; Transferase; Transmembrane.
SEQUENCE 527 AA; 59657 MW; 6607C24551D3B9E9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.2e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.3%; Score 2109; 75.8%; Pred. No. 2.
InterPro; IPR000472; Activin_receptor. InterPro; IPR00333; Activin_receptorII. InterPro; IPR00319; Prot_kinase. InterPro; IPR008271; Ser_thr_pkin_AS. InterPro; IPR003605; TGFDetarccept_GS. Pfam; PF00164; Activin_recp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment).
ORFNames=GSTENG00034592001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 402; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TETNG PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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EMARKCVTGGIVEEYQLPYWDWVPSEPSYEDMREVVCVKSMRPVVSNRWNSDECLRVMLK 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIPGKPPFWNAHL--LAFLISVIVCCFTLVAI-TIVCYYRF-KLQTGRRHYQRDLGPIEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 VVIG--PFFDGSVRWLAVLISMAVCIVAMIVFSSCFCYKHYCKSISSRGRYNRDLEQDEA
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R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004674; F:protein serino/threonine kinase activity; IEA.

R GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

R GO; GO:0005024; F:transforming growth factor beta receptor ac. ..;

R GO; GO:0005648; F:protein amino acid phosphorylation; IEA.

R InterPro; IPR000472; Activin receptor.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR002290; Ser thr pkin AS.

R InterPro; IPR002290; Ser thr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R Pfam; PF01064; Activin recp; 1.

R Pfam; PF01064; Prinase; 1.

R Pfam; PF00069; Pkinase; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-TREB-2005 (TrEMBLrel. 29, Last annotation update)
Bone morphogenetic protein receptor type IB (Bone morphogenetic
                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 534;
                                                                                                                                                                                                                               SMART; SM00467; GS; 1.
SMART; SM00202; S TKC; 1.
SMART; SM00219; TVKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nuclectide-binding; Receptor;
Serine/threonine-protein kinase; Transferase; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                   534 AA; 59781 MW; FF0B38D40DA3C212 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   74.2%; Score 2104.5; DB 2 77.2%; Pred. No. 4.6e-137;
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O9BDI4;
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A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Altschul S.F., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brantchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raden J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,
Butterfield W. Schwinski M.I., Skalska U., Smailus D.E.,
Butterfield S., Solmitlal analysis of more than 15,000 full-length human
                                                                                                                                                                     438
                                                                                                                                                                                                    405
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   166 FIPAGESLRDLIHQSQSSGSGSGLPLLVQRTIAKQIQMMRQIGKGRYGEVWLGRWRGEKV 225
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                                                                                                                     ADLGLAVKFNSDTNEVDIPLNTRVGTRRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIW
                                                                                                                                                                                                                                   EMARRCITGGIVEEYOLPYYNMVPSDPSYEDMREVVCVKRLRPIVSNRWNSDECLRAVLK
                                   AVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLY
                                                                                                   DPLKCATLDTRALLKLAYSAACGLCHLHTEIYGTQGKPAIAHRDLKSKNILIKKNGSCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OŘFNames=zgc:92227;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rero (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                  LMSECWAHNPASRLTALRIKKTLAKMVESQDVKI 532
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ZFIN; ZDB-GENE-040912-150; zgc:92227.
GO; GO:0016020; C:membrane; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                             Q66HY1_BRARE PRELIMINARY;
Q66HY1;
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DDQGETTLTSGCMKYEGSDFQCKDSPKAQLRRTIECC-RTNLCNQYLQPTLPPVVIGPFF 147
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                                                                                                                                                                                       DLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQVGKGRYGEVWMGKWRGEKVAVKVFFTTE
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                                                                                                                                    Gaps
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                                                                                                  502;
                                                    Transmembrane
                                                                                                  Length
                                                                                                                ; Pred. No. 1.9e-126;
58; Mismatches 75; Indels
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nuclectide-Einding; Receptor; Serine/threonine-protein kinase; Transferase; Transmemt SEQUENCE 502 AA; 56907 MW; 6552124A0A24F35C CRC64;
                                                                                                  DB 2;
                                                                                                Query Match 68.7%; Score 1950.5; Best Local Similarity 72.7%; Pred. No. 1.9e Matches 367; Conservative 58; Mismatches
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000504; F:transforming growth factor beta receptor ac. . .; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
GO; GO:0007178; P:transmembrane receptor protein serine/threo. . ; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with
                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson T., Wu X.Y., Juengel J.L., Ross I.K., Lumsden J.M., Lord E.A., Dodds K.G., Walling G.A., McEwan J.C., O'Connell A.R., McNatty K.P., Montgomery G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Highly prolific Booroola sheep have a mutation in the intracellular kinase domain of bone morphogenetic protein IB receptor (ALK-6) that is expressed in both oocytes and granulosa cells.", Biol. Reprod. 64:1225-1235(2001).
                                                                                                                                                                                                                 the
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Proc. Natl. Acad. Sci. U.S.A. 98:5104-5109(2001).

-! SUBUNIT: Interacts with AIPI. Part of a complex consisting of AIPI, ACVR2, ACVRB and MADH3 (By similarity).

-! SUBCELULAR LOCATION: Type I membrane protein (By similarity).

-! SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AF357007; AAK30296.1; -; mRNA.

EMBL; AF312016; AAK487091; -; mRNA.
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                           Ovigo aries (Sheep).

Bukaryos aries (Sheep).

Bukaryos, Metazos, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                              MEDLINE=21211518; PubMed=11312159; DOI=10.1677/joe.0.169R001; Souza C.J., MacDougall C., Campbell B.K., McNeilly A.S., Baird D.T.; "The Booroola (FecB) phenotype is associated with a mutation in bone morphogenetic receptor type 1 B (BMPR1B) gene."; J. Endocrinol. 169:R1-R6(2001).
                                                                                                                                                                                                                                                                                                                 T., Telfer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson T.M., Ross I.K.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00107; PROTEIN KINASE ATP; 1.
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InterPro; IPR00033; Actn_receptorII.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR003605; TGFDetarecept_GS.
                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Ovary;
MEDLINE=21159170; PubMed=11259271;
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ProDom; PD000001; Prot_kinase; 1.
SMART; SM00467; GS; 1.
                                                                              Pecora; Bovidae; Caprinae; Ovis.
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Pfam; PF00069; Pkinase; 1.
 protein type 1B receptor)
Name=BMPR-1B;
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Title: Perfect score:

Sequence:

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Scoring table:

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Minimum Maximum

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RATRB4R1 1599 bp mRNA linear ROD 04-FEB-1999 Rat mRNA for bone merphogenetic protein 4 receptor, complete cds. D17667
                                                                                                                                                                                                                                                                                                                                                          ARI44415 Sequence
ARI74013 Sequence
BD191976 The use o
U04673 Mus musculu
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A3809 Sequence
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ARI64270 Sequence
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AR264348 Sequence
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AR26334 Hsapiens A
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C21535 Hsapiens A
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CQ986811 Sequence
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CS027156 Sequence
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A23814 M.musculus
A38817 Sequence 13
AR140650 Sequence
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Submitted (16-SEP-1993) Hiroshi Takahashi, Tokyo Metropolitan
Institute of Gerontology, Department of Pathology; 35-2 Sakaecho,,
Itabashi-ku, Tokyo 173, Japan (Tel:03-3964-3241(ex.3034),
Fax:03-3579-4776)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Makaryota, Metazoa, Eusenbortoglires, Glires, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.

1. (Dases 1 to 1599)

Ikeda, T. and Takahashi, H.

Expression pattern of bone merphogenetic protein 4 receptor in embryo and adult rat
Unpublished
CQ986812 Sequence
CS027157 Sequence
D38082 Rat mRNA fo
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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MWU04672
BC042611
MWU04673
CQ848002
AR1740646
AR1740646
AR164270
CQ986807
CQ986807
AR263383
CQ718018
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Takahashi, H.
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TITLE
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AUTHORS
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         Command line parameters:
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-DB-GenEmbl.-QFWT=factap.-SUFFTX=rge.-MINNATCH=0.1.-LOOFCL=0.-LOOFEXT=0
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AR169902 Sequence
AR382508 Sequence
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                 - nucleic search, using frame_plus_p2n model
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                               CCAGTAGGAGAATCACTGAAAGACCTGATTGACCAGTCACAAAGCTCTGGTAGTGGATCT
                                                     laLysGlnIleGlnMetValArgGlnVal
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                                                                                              GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
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Genetics Institute, LLC.; Cambridge,
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                                                                    ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro
                                                                                                                          ValValleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet
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EKYQLPYYNWYPSDESYENDHEVVCVKRLRPIVSNRMNSDECLRAVLKLMSECWAHNP
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Submitted (26-AUG-1994) Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental University, Department of Biochemistry; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)
On Jun 29, 1996 this sequence version replaced gi:599585.
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Db 1666 CCAATCGTCTCTAACCGCTGGAACAGTGATGTCTTCGAGCCGTTTTGAAGCTGATG 1725	CS027155 LOCUS DEFINITION Sequence 88 from Patent W02005014650. DEFINITION Sequence 88 from Patent W02005014650. DEFINITION CS027155 GENERAL SEQUENCE SOURCE SOURCE ORGANISM Rattus Sp. ORGANISM Rattus Sp. Mammalia, Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	AUTHORS Winkler, D.G., Shi, J. and Latham, J. TITLE Antibodies specific for sclerostin and methods for increasing bone mineralization later wo 2005014650-A 88 17-FEB-2005; Callech R & D, Inc. (US) Callech R & D, Inc. (US) Callech R & D, Inc. (US) Collech R & D, Inc. (US) Collech R & D, Inc. (US) Acadion/Qualifiers 1. 3167 /organism="Rattus sp." /mol type="unassigned DNA" /db_xref="taxon:10118"	Alignment Scores: 9.15e-271 Length: 3167 Pred. No.: 2838.00 Matches: 532 Score: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Ouery Match: 6 Gaps: 0	-10-600-645-2 (1-532) x CS027155 (1-3167) 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20	286 GTTCAAGGGCAGAATCIAGATAGIATGCTCCATGGTACTGGTATGAAATCAGACGTGGCAC 34 41 GlnLysLysProGludsnGlyvalThrLeualaProGludspThrLeuProPheLeuLys 60	406 TGCTATTGCTCAGGACACTGCCCAGATGACGCTATTAATAACACATGCATAACTAATGGC 465 Qy 81 HisCysPhealaileileGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100 466 CATTGCTTTGCCATTATAGAAGATGATGAGGAGAAACTCTTGGGTGT 525 Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProlysAlaGlnLeuArgArg 120 Db 526 ATGAAGTATGAGAGCTCTGATTTTCAATGAAGGATTCACCAGAAGCCCAGCTAGCGGG 585 Qy 121 ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140 586 ACAATAGAAGTTGTCGGACCAATTTGTGCAACCAAAGCCTACACCCCCT 645

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	Extervolus by Detazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 3167) AUTHORS Takeda, K. TITLE Expression of serine/threonine kinase receptors during ectopic bone formation induced by bone morphogenetic protein (BMP)	COCKARD ANALOG GAKKAI ZABBIL b1 (4), 512-526 (1994) PUBMED 7897267 REWARK GenBank staff at the National Library of Medicine created this REMARK GenBank staff at the National Library of Medicine created this REMARK GenBank staffs from the original journal article. FEATURES 1. 3167 (Qualifiers 1. 3167 (Anganism="Rattus sp.") //mol type="MRNA"	receptor,	/gene="bone morphogenetic protein type IA receptor, BMP type IA receptor, BMPR-IA" /note="BMP type IA receptor; BMPR-IA" /codon_start=1 /product="bone morphogenetic protein type IA receptor" /protein id="AAB33865.1" /db_xref="G1:834008"	VICTAINS AS TO THE WAS TO THE LIGHT TO THE MEDICAL THE SECRET TO THE SECRET TO THE SECRET SECRET THE SECRET TH	Alignment Scores: 9.15e-271 Length: 3167 Score: 2838.00 Matches: 532 Score: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Indels: 0 DB: 200.00\$ Caps: 0	US-10-600-645-2 (1-532) x S75359 (1-3167) Qy

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                                                                                                                                         2 (bases 1 to 1599)
Miyazono,K.
Direct Submission
Submitted (25-JUN-1993) Kohei Miyazono, Ludwig Institute for Cancer
Research, Biomedical, Center, Uppsala, S-751 24, Sweden
Location/Qualifiers
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Distinct spatial and temporal expression patterns of two type I
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/dev stage="12 day embryo"
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Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                           ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspCluSerLeuSerLysAsn
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Miyazono, K., ten Dijke, P., Franzen, P., Yamashita, H.
Heldin, C.-H.
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Patent: US 6207814-A 13 27-MAR-2001;
Location/Qualifiers
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-Q=/cgn2_1/USPTO spool/US10600645/runat_02122005_103604_23270/app_query.fasta_1.711
-DB=N Geneseq -QFMT=Fastap -SUFPIX=rng -MINMATCH=0.1 -LÖOPEX=0 -LIOSPEX=0
-UNITZ=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-USRE=US10600645_@CGN 1 1.542_@runat_0212205_103604_23270 -NCPU=6 -ICPU=3
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                        Truncated bone morphogenic protein (BMP) receptors and serine/threonine kinase receptors may be used in compositions to inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated receptors pref. comprise the ligand binding domain, but not the serine/threonine kinase and transmembrane domains. The truncated proteins are soluble and will be excreted into supernatant by recombinant mammalian cells expressing them. Such cells can be delivered in a medium or matrix which partially impedes their mobility, thereby localising the cells to a site of bone or cartilage injury. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                    Truncated BMP and serine/threonine kinase receptor proteins - inhibit the effects of BMP-2 and/or BMP-4.
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invention can be used for treating osteopenia, osteoporosis, fractures and other disorders related to low bone mineral content and density. As such, these compositions improve bone mineralization and can be described as TGF-beta antagonists and/ or BMP-antagonists. This polynucleotide is a bone morphogenetic protein receptor type I DNA sequence given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel antibody or antigen-binding fragment that binds specifically to a sclerostin (SOST) polypeptide and impairs formation of a sclerostin homodimer. Specifically, it refers to an antibody that competitively inhibits binding of the sclerostin polypeptide to a bone morphogenic protein (BMP) Type I receptor binding site or a BMP Type II receptor binding site or a BMP type II receptor binding site. The present invention describes a hybridoma cell capable of producing the antibody and a host cell for antibody expression. Furthermore, it provides a nucleic acid molecule encoding a transforming growth factor-beta (TGP-beta) binding protein known as SOST (and also BEER) and methods for detection thereof.
                                                                                                                         receptor; bone morphogenetic protein; bone injury; antibody production; TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibody or antigen-binding fragment that binds specifically to sclerostin polypeptide and which inhibits binding of sclerostin polypeptide to a bone mothy polypeptide to a bone mothy mineral content or density.
                                                                                        Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seg 121
                                                                                                                                                                                                                                                   83. .1681 /
/*tag= a
/product= "BMP receptor type 1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mulligan JT,
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                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-2003; 2003US-00463190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CLLT ) CELLTECH R & D INC
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galas DJ,
Winkler DG;
                                                                                                                                                             osteoporosis; gene; ds.
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P-PSDB; ADW28803.
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Van Ness J,
                  ADW28817;
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.; BM:

Paeper

U; 0 Other 0 ÷ Sequence 3003 BP; 840 A; 626 C; 654 G; 883

9.23e-294

Score: Percent Similarity: Pest Local Similarity: Query Match:	2838.00 100.00% 100.00% 100.00%	Matches: Conservative: Mismatches: Indels: Gaps:	000000000000000000000000000000000000000
US-10-600-645-2 (1-532) x ADW28817 (1-3003)	x ADW28817	(1-3003)	

MetThrGlnLeuTyrThrTyrlleArgLeuLeuGlyAlaCysLeuPhellelleSerHis 20

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340 120 140 160 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180 320 262 322 100 382 442 502 562 622 200 682 220 742 802 260 862 280 922 300 80 GTTCAAGGGCAGAATCTAGATAGTATGCTCCCATGGTACTGGAATGAAATCAGGACGTGGAC HisÇysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys CATTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAAACCACGTTAACTTCTGGGTGT MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 863 AAAGTATTTTTACCACTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACG GTGTTAATGCGTCATGAAAATATACTTGGTTTTATAAGCTGCAGACATTAAAGGCACCGGT SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 1163 cgagaccrgaagggaaaaacarccrrarraagaaaarggragrrgcrgrarrgcrgac ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer ccagraegagarcacreaagaccrearreaccagreacaagcreregraegearer GGATTACCTTTATTGGTTCAGCGAACTATTGCCAAACAGATTCAGATGGTTCGGCAGGTT GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal GGTAAAGGCCGGTATGGAGAAGTATGGATGGGTAAATGGCGTGGTGAAAAAGTGGCTGTC ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly TCCTGGACTCAGCTGTATTTGATTACTGATTACCATGAGAATGGGTCTCTCTATGACTTC LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys CTGAAATGTGCCACCCTGGACACCAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 383 443 161 683 743 1043 361 21 143 41 203 263 923 301 321 341 61 81 323 101 121 141 503 563 181 623 201 241 803 261 281 983 1103 221 g ò ద g g 셤 ò g g 임 ò g g QQ g 셤 엄 셤 ò ò 셤 à 8 8 8 ò ò ò ò à à ò 셤 ò ò

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/*tag= a
/product= "Rat bone morphogenic protein type I receptor"
                                                          1343 CATTICCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTTGGTTTGGGAGATG
            1223 CTGGGCCTAGCTGTTAAATTCAACAGTGACACAAAATGAAGTTGACATACCCTTGAACAC
                                                                                                                                                                                                                                                     1523 CCAATCGTCTCTAACCGCTGGAACACTGATGATGTCTTCGAGCCGTTTTGAAGCTGATG
                                                                                                                                                                                                                                                                                   SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArg1leLysLysThr
                                                                                                                                                                                                                                                                                                       1583 TCAGAATGCTGGGCCCATAATCCAGCATCCAGACTCACAGCTTTGAGAATCAAGAAGACG
LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr
                                             ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn
                                                                                          421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet
                                                                                                                                         AlaArgArgCys1leThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet
                                                                                                                                                                                        Val ProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg
                                                                                                                                                                                                                ProlleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody; sclerostin; SOST; bone morphogenic protein receptor; Transforming Growth Factor; osteopathic; gene therapy; bone repair; osteopenia; osteoporosis; bone injury; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     norvegicus.
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The invention relates to a novel isolated antibody, or its antigenbinding fragment, which binds specifically to a sclerostin (SOST) polypeptide comprises any of 6 sequences having 190 or 213 amino acids, fully defined in the specification (ADX97341, Cor 213 amino acids, fully defined in the specification (ADX97341, Cor 2009ctlitively inhibits binding of the SOST polypeptide to a bone competitively inhibits binding of the SOST polypeptide to a bone competitively inhibits binding of the SOST polypeptide to a bone comprises a hybridoma cell producing the new antibody; a composition of further comprises a hybridoma cell producing the new antibody; a host cell that is capable of expressing the new antibody; a composition of further comprises a hybridoma cell producing the new antibody; a host cell that is capable of expressing the new antibody; a composition of physiological carrier; an immunogen comprising a peptide composition of physiological carrier; an immunogen comprising a peptide composition of physiological carrier; an immunogen comprising a peptide comprising of physiological carrier; an immunogen comprising a peptide compositionly between the SOST polypeptide; and methods for identifying an antibody that specifically that impairs binding of a BMP to the SOST polypeptide, that impairs SOST compositions have osteopathic activity. The SOST nucleic acids may be used in gene therapy. The composition and methods are useful correasing bone mineralization, which may treat or prevent diseases or conditions associated with low bone mineral density, such as conditions associated with low bone mineral density, such as expressed in the morphogenic protein type I receptor encoding DNA of the invent; and the such in the morphogenic protein type I receptor encoding DNA of the invent; and the such is protein type I receptor encoding DNA of the invent; and the such in the such protein type I receptor encoding DNA of the invent; and the such protein type I receptor encoding DNA of the invent; and the such protein type I rec
                              Disclosure; SEQ ID NO 90; 157pp; English
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T; 0 U; 0 Other; BP; 840 A; 626 C; 654 G; 883 Sequence 3003

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          Length:
Matches:
Conservative:
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Gaps:
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          9.23e-294
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Alignment Scores:
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GTCGTFATAGGCCCATTCTTTGATGGCAGCGTCCGATGGCTGGGTGTGCTCTTTTTTTAGT

ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet

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New isolated antibody specific for a sclerostin polypeptide, useful for increasing bone mineralization or for treating or preventing conditions associated with low bone mineral density, e.g. osteoporosis or

osteopenia

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       AlaValCys1eValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys
                  GCTGTCTGTATTGTCGCCATGATCGTCTTCTCCCAGCTGCTTCTGTTACAAACATTACTGT
                                         LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle
                                                                           ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerGlySerGlySer
                                                                                     GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal
                                                                                                                        GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal
                                                                                                                                                           AAAGTATTTTTTACCACTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACG
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                                                         AAGAGTATCTCAAGCAGAGGTCGTTACAACCGTGACTTGGAACAGGATGAAGCATTTATT
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This invention relates to a novel antibody or antigen-binding fragment that binds specifically to a sclerostin (SOST) polypeptide and impairs formation of a sclerostin hondowner. Specifically, it refers to an antibody that competitively inhibits binding of the sclerostin cantibody that competitively inhibits binding of the sclerostin polypeptide to a bone morphogenic protein (BMP) Type I receptor binding site or a BMP Type II receptor binding site. The present invention describes a hybridoma cell capable of producing the antibody and a host cell for antibody expression. Furthermore, it provides a nucleic acid confecule encoding a transforming growth factor-beta (TGF-beta) binding protein known as SOST (and also BEER) and methods for detection thereof. Accordingly, such antibodies and osteopathic compositions of the and other disorders related to low bone mineral content and density. As such, these compositions improve bone mineral content and density. As such, these compositions improve bone mineral content and density. As such, these compositions improve bone mineral content and can be described as a TGF-beta antagonists. This polymolectide is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor; bone morphogenetic protein; bone injury; antibody production; TGF beta antagonist; BMP-antagonist; osteopenias; osteoporosis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody or antigen-binding fragment that binds specifically to sclerostin polypeptide and which inhibits binding of sclerostin polypeptide to a bone morphogenic protein, useful for increasing bone mineral content or density.
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Van Ness J, Winkler DG;
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P-PSDB; ADW28802.
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New antibody or antigen-binding fragment that binds specifically to sclerostin polypeptide and which inhibits binding of sclerostin polypeptide to a bone morphogenic protein, useful for increasing bone mineral content or density. Disclosure; SEQ ID NO 119; 205pp; English.

invention can be used for treating osteopenia, osteoporosis, fractures and other disorders related to low bone mineral content and density. As such, these compositions improve bone mineralization and can be described as TGF-beta antagonists and/ or BMP-antagonists. This polynucleotide is a that binds specifically to a sclerostin (SOST) polypeptide and impairs formation of a sclerostin homodimer. Specifically, it refers to an antibody that competitively inhibits binding of the sclerostin polypeptide to a bone morphogenic protein (BMP) Type I receptor binding site or. a BMP Type II receptor binding site. The present invention describes a hybridoma cell capable of producing the antibody and a host cell for antibody expression. Furthermore, it provides a nucleic acid molecule encoding a transforming growth factor-beta (TGF-beta) binding protein known as SOST (and also BEER) and methods for detection thereof. Accordingly, such antibodies and osteopathic compositions of the bone morphogenetic protein receptor type 1 DNA sequence given in an exemplification of the invention. invention relates to a novel antibody or antigen-binding

Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

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MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp GTTCAAGGGCAGAATCTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC CAGAAGAAGCCGGAAAATGGAGTGACGTTAGCACCAGAGGACACCTTACCTTTATAAA HisCysPheAlalleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys CATTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAAACCAGGTTAACTTCTGGGTGT ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCAGCTACGCAGC ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys TGCTATTGCTCAGGACACTGCCCAGATGACGCTATTAATAACACATGCATAACTAATGGC MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg CysTyrCysSerGlyHisCysProAspAspAlalleAsnAsnThrCysIleThrAsnGly 3167 532 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-10-600-645-2 (1-532) x ADW28815 (1-3167) 9.99e-294 2838.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: 226 21 286 41 346 406 81 466 101 526 121 61 586 141 646 Query Match: DB: ઠ 셤 ò g g ò 유 유 В g ð ò ò ò ò

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CC binding fragment, which binds specifically to a sclerostin (SOST)

CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190

CC or 213 amino acids, fully defined in the specification (ADX97341,

CADX97360, ADX97398, ADX97400 to ADX97408). The antibody

CC competitively inhibits binding of the SOST polypeptide to a bone

morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II

CC capable of binding to a BMP Type I Receptor binding site is

CC capable of binding to a BMP Type I Receptor binding site is

CC capable of binding to a BMP Type I Receptor binding site is

CC capable of binding to a BMP Type I Receptor binding site is

CC capable of binding to a BMP Type I Receptor binding site is

CC capable of binding to a BMP Type I Receptor binding site is

CC further comprises: a hybridoma cell producing the new antibody; a host

CC comprising the new antibody, or its antigen-binding fragment, and a

CC phygiological carrier; an immunogen comprising a peptide comprising 6, 7,

CC the SOST polypeptide; and methods for producing an antibody that specifically

CC that modulates a Transforming Growth Factor (TGF)-been signaling pathway,

CC that modulates a Transforming Growth Factor (TGF)-been signaling pathway,

CC that modulates a Transforming of a BMP to the SOST polypeptide, that impairs SOST homodimer formation, or that increases bone mineral content. The novel

Antibody and compositions have osteopathic activity. The SOST nucleic

C acids may be used in gene therapy. The composition and methods are useful

C or conditions associated with low bone mineral density, such as

C represents a rat bone morphogenic protein type I receptor encoding DNA of

C the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Rat bone morphogenic protein type I receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated antibody specific for a sclerostin polypeptide, useful for increasing bone mineralization or for treating or preventing conditions associated with low bone mineral density, e.g. osteoporosis or
                                                                                                                                                                                                                                                                                                                                                antibody; sclerostin; SOST; bone morphogenic protein receptor;
Transforming Growth Factor; osteopathic; gene therapy; bone repair;
osteopenia; osteoporosis; bone injury; gene; ds.
                                                                                                                                                                                                                                                                                                Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID
Disclosure; SEQ ID NO 88; 157pp; English.
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P-PSDB; ADX97414.
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Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;
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New isolated antibody specific for a sclerostin polypeptide, useful for increasing bone mineralization or for treating or preventing conditions associated with low bone mineral density, e.g. osteoporosis or
               16-JUN-2003; 2003US-0478977P.
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/product= "Rat bone morphogenic protein type I receptor"
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The invention relates to a novel isolated antibody, or its antigenbinding fragment, which binds specifically to a sclerostin (SOST)

CC binding fragment, which binds specifically to a sclerostin (SOST)

CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190

or 213 amino acids, fully defined in the specification (ADX97341,

CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody

CC competitively inhibits binding of the SOST polypeptide to a bone

morphogenic protein (BMP) Type I Receptor binding site is

Receptor binding site, where the BMP Type I Receptor binding site is

capable of binding to a BMP Type I Receptor binding site is

Receptor binding to a BMP Type I Receptor binding site is

capable of binding to a BMP Type I Receptor polypeptide. The invention

further comprises: a hybridoma cell producing the new antibody; a host

cell that is capable of expressing the new antibody; a composition

comprising the new antibody, or its antigen-binding fragment, and a

physiological carrier; an immunogen comprising a peptide composition

CC ell that is capable of expressing corrective amino acids of

the SOST polypeptide; methods for producing an antibody that specifically

comprising the new antibody or its antigen-binding fragment, the novel

that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,

that impairs binding of a BMP to the SOST polypeptide, that impairs SOST

composition and methods and composition and methods and underly and composition and methods in gene therapy. The composition and methods are useful

caids may be used in gene therapy. The composition and methods are useful

conficients associated with low bone mineral density, such as

costeopenia, osteoporosis or bone fractures. This polynucleotide sequence

represents a rat bone morphogenic protein type I receptor encoding DNA of

the invention.
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                                                                                 CCAATCGTCTCTAACCGCTGGAACAGTGATGAATGTCTTCGAGCCGTTTTGAAGCTGATG
                                                                                                                            ProlleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activin receptor-like kinase(s) with serine/threonine kinase domair have activin/TGF beta-type I receptor function and can be used in diagnosis or therapy or rheumatoid arthritis, glomerular nephritis,
                                                                                                                                                                                                                                                                                                                                     serine threonine kinases, activin receptors; Act-R; superfamily, transforming growth factor; TGF; diagnostics; detection; therapy; rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
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                                                    ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCCAGCTACGCAGG
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ce activin receptor-like kinases (ALK). Their discovery was based on the realisation that receptor serine/threonine kinases form a new receptor femily, which may include the type II receptors for other proteins in the transforming growth factor (TGF) beta superfamily. The activin receptor type II sequences from mouse and the dafi gene product of C.elegans have high sequence similarity and were used to design degenerate primers to clone related cDNA's (see AAQ66631-49). Six distinct putative receptor serine/threonine kinases (ALK 1-6, of which human ALK 1-5 are AAQ66631-38 respectively, and the mouse ALK-1,3,4, and 6 are AAQ66639-4 respectively) were identified mALK-3 cDNA as a probe. Two overlapping clones were identified that together covered the complete sequence of mALK-3. Products of the invention can be used in therapy, eg. to modulate conditions associated with activin or TGF beta activity. These conditions theumatoid arthritis and glomeronephritis. (Updated on 25-MAR-2003 to correct PN field.)
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                        mALK-3; activin receptor-like kinase; therapy; activin; TGF-beta; cancer; fibrosis; liver cirrhosis; pulmonary fibrosis; glomerulonephritis; mouse; rheumatoid arthritis; detection; diagnosis; drug screening; ds.
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treating e.g. fibrosis, cancer, rheumatoid arthritis and
glomerulonephritis.
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Mismatches:
Indels:
Gaps:
mALK-3 from clone ME-7 and ME-D cDNA
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acids and the encoded proteins thereof. Specifically, it refers to receptor kinases identified as activin receptor like kinases (Alks) that are members of the transforming growth factor beta (TGF-beta) superfamily. The present invention describes a method for identifying TGF-beta inhibitors by determining whether a substance is an antibody that TGF-beta or Alk-1, in particular where that substance is an antibody that binds to TGF-beta or the extracellular domain of Alk-1. The proteins having specific serine/ threonine receptor kinase activity can be used in therapy to modulate activin or TGF-beta activity and as such can be used to treat liver cirrhosis and pulmonary fibrosis, cancer, rheumatoid arthritis or glomerulonephritis. Accordingly, they exhibit hepatotropic, antiinflammatory, respiratory-Gen, cytostatic, antirheumatic, antiarthritic and nephrotrepic activities. This polynucleotide is the murine Alk CDNA secuence of the invarior.
                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGAAGAAGCCAGAAAATGGAGTGACTTTAGCACCAGAGGATACCTTGCCTTTCTTAAAG 396
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                                                                                                                                                                                                                                                                                                                                               gene; 88; antibody production; serine-threonine kinase receptor; activul like kinase; transforming growth factor beta; liver cirrhosis; pulmonary fibrosis; cancer; rheumatoid arthritis; glomerulonephritis; hepatotropic; antilnflammatory; respiratory-gen.; cytostatic; antirheumatic; antiarthritic; nephrotropic.
               CAATCGTGTCTAACCGCTGGAACAGCGATGAATGTCTTCGAGCAGTTTTGAAGCTAATG
                                                  ProllevalSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet
                                                                                                       SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArglleLysELysThr
Val ProSerAspProSerTyrGluAspMetArgGluValValValCysValLysArgLeuArg
                                                                                                                                                         Murine ALK-3 cDNA (clones ME-7 & ME-D) Seg 13.
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93WG-CB002367.
95WS-00436265.
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(IMAM/) IMAMURA T.
(TDIJ/) TEN DIJKE P
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TEN DIJKE
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03-AUG-1993;
15-OCT-1993;
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Query Match:
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                                                    LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr
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               GlyLysGlyArgTyrGlyGluValTrpWetGlyLysTrpArgGlyGluLysValAlaVal
                                                                                      ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bone morphogenetic protein receptor kinase protein - used for identifying cpds. capable of binding it and for developing therapeutic cpds. and detection system(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A cDNA library prepared from NIH3T3 poly-A RNA was screened with J159 | fragment to isolate clone BRK-1 (sequence given in AAQ90184) encoding full-length BMP receptor Kinase protein (AAR74343). Vectors including 1DNA were used to express recombinant BRK-1 in CHO and COS-7 hosts. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValG1nG1vG1nAsnLeuAspSerMetLeuHisG1yThrG1yMetLysSerAspValAsp
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ds.
receptor kinase protein-1; bone morphogenetic protein;
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The sequence encodes mouse bone morphogenetic protein (BMP) receptor type -I kinase-1 (BRK-1), which induces cellular differentiation in response to BMP. The gene may be inserted in plasmid pJT4, to form plasmid pJT4-J159F, and co-expressed with a type-II BRK-3 gene to study complex formation between the 2 receptor types. The BRK-3 receptor and antibodies against it may be used in diagnostic assays for BMP disorders, or in therapy to bind or scavenge BMPs. In addition, expression of the BRK-3 gene along with a reporter gene under the control of a hormone-responsive element in a cell culture may be used to screen compounds for BRK-agonist or -antagonist activity, by monitoring reporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "Bone morphogenetic protein receptor kinase-1"
                                                                                                             CCAATCGTGTCTAACCGCTGGAACAGCGATGAATGTCTTCGAGCAGTTTTGAAGCTAATG
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                                                                                        SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                   bone morphogenetic protein receptor kinase-3; antibody, diagnostic; bone disorder; osteogenic; bone morphogenetic protein-agonist; drug screening; reporter gene; bone morphogenetic protein-antagonist; drug screening; responsive element; ds.
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                                                                                          A cDNA clone (AAT28021) codes for full-length mouse bone morphogenetic protein (BMP) type I receptor kinase protein-1 (BRK-1) (AAR95225), a receptor capable of binding BMP and transdeducing a signal intitated by the binding. Host cells co-transfected with vectors carrying full-length, incomplete or soluble BMP type I receptor kinase protein cDNA and full-bingth, incomplete, soluble or truncated BMP type II receptor kinase protein.3 (BRK-3) cDNA (See also AAT28018-20 and AAT28022-30) express a BMP receptor complex useful for screening cpds. for BMP receptor affinity or for determining the concentration of a BMP receptor ligand in a
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                                              morphogenetic protein activities - using complex of B kinase protein and BMP receptor kinase protein BRR-3.
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                                                                                                                                                                                                      Sequence 2402 BP;
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                                              Assays for bone type I receptor
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 Rosenbaum JS;
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                                                                                                                                                                                                                                                                                                                                                              This cDNA encodes a mouse BMP receptor kinase protein (BRK)-1. This can be used in the method of the invention of determining whether a compound can bind to a bone morphogenetic protein (BMP) receptor kinase protein complex. The method comprises allowing a compound in a sample to bind to the complex, where the complex is comprised of (i) a BMP; (ii) a BRK protein; (iii) an ActRIIB receptor. The method can be used to determine the concentration of a BMP receptor ligand in a sample by comparing the binding to a standard curve prepared with known concentrations of BMP ligand. The method can also be used to determine whether a test compound produces a signal on binding to a BMP receptor protein complex. The method is useful for determining whether a ligand, such as a known or putative drug, can bind to and/or activate the receptors
                                                                                                                                                                                                                                                                                                     Screening method using bone morphogenetic protein receptor complex - which binds to potential drugs, and ActRIIB receptor used in the complex, also host cells transfected with DNA encoding the complex.
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                                                morphogenetic protein; BMP; BMP receptor kinase; ActRIIB receptor; receptor ligand; drug; ds.
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                              Mouse BMP receptor kinase protein (BRK)-1 encoding cDNA
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        to correct PN field.)
                                   G; 541 T; 0 U; 0 Other;
                                                                          2056
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                                                                         Length:
Matches:
Conservative:
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       (Updated on 25-MAR-2003
                                                                                                                                                                          US-10-600-645-2 (1-532) x AAQ90183 (1-2056)
                                 573 A; 436 C; 506
                                                                          1.04e-289
2798.00
94.48%
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                                 BP;
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Best Local Similarity:
       COS-7 hosts.
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                                                             Alignment Scores:
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New bone morphogenetic protein receptor kinase protein - used for identifying cpds. capable of binding it and for developing therapeutic cpds. and detection {\rm system}(s).
                                                          GCTCGTCGTTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATG
                                                                                               ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg
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                                       AlaargargcysilethrGlyGlyileValGluGluTyrGlnLeuProTyrTyrAsmMet
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291. .1793
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P-PSDB; AAR74342.
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Search completed: December 9, 2005, 19:48:47 Job time : 662 8ecs

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MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Felease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LAZAK, Steven R
REGISTRATION NUMBER: 32,618
REGISTRATION NUMBER: 32,618
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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US-08-158-735A-3

US-08-138-735A-1

US-08-131-179A-11

US-08-131-137A-1

US-09-382-256-5

US-09-382-256-5

US-09-395-115-5

US-09-64-171A-5

US-09-949-016-1914

US-09-949-016-1914

US-09-949-016-13188

US-09-949-016-13188

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US-09-131-17

US-08-46-265-17

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US-08-46-265-17

US-08-46-265-17

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US-08-46-265-17

US-08-46-265-17

US-08-46-263-1

US-09-134-10080-3

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US-09-395-115-9
US-08-436-265-9
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Patent No. 6291206

GENERAL INFORMATION:
APPLICANT: WOZNEY, John
APPLICANT: THEST, R. Scott
APPLICANT: MAMAJI, No. 6291206oru
APPLICANT: YAMAJI, No. 6291206oru
APPLICANT: THEST, R. SCOTT
APPLICANT: APPLICANT
APPLICANT: THEST, R. SCOTT
APPLICANT: SAMAJIGGEPATK DIIVE
APPLICANT: CambridgePark Drive
CONTY: Cambridge
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COUNTRY: USA
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Sequence 13,
Sequence 11,
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-874-628-1
PCT-US94-10080-1
US-09-382-256-13
US-08-395-115-13
US-08-436-265-13
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Listing first 45 summaries
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Sequence 1, Application US/09874628
Patent No. 6610513
GENERAL INFORMATION:
GELESTE, Anthony J.
THIES, R. SCOCCT
THIES, R. SCOCCT
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Legal Affairs
                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAlaLysMetValGluSerGlnAspValLysIle
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US-09-874-628-1
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Matches:
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Indels:
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TELEFAX: 617 876 5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANNEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: CFK1-23a
FRATURE:
                                                                                                                               1.28e-317
2838.00
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                                                                                           ; NAME/KEY: CDS
; LOCATION: 61..1656
US-08-123-934A-1
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Best Local Similarity:
Query Match:
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                                                        AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys
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                GCTGTCTGTATTGTCGCCATGATCGTCTTCTCCCAGCTGCTTCTGTTACAAACATTACTGT
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                                                   ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: OS-JUN-2001
CLASSIFICATION NUMBER: US/09/874,628
FILING DATE: OS-JUN-2001
RIOM APPLICATION NUMBER: 08/123,934
FILING DATE: 17-SEP-1993
ATTORNEY/AGENT: INFERMATION:
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Matches:
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Gaps:
STREBT: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                     NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REPERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEFANE: 617 876 1170
TELEFAX: 617 876 5851
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 61..1656
SEQUENCE DESCRIPTION: SEQ ID NO:
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TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
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CCAATCGTCTCTAACCGCTGGAACAGTGATGAATGTCTTCGAGCCGTTTTGAAGCTGATG 1560
                                  Sequence 1, Application PC/TUS9410080
GENERAL INFORMATION:
APPLICANT: GENETAL INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: 87 CambridgePark Drive
CITY: CambridgePark Drive
STATE: MA
COUNTRY: USA
COMPUTER: ENDAY
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10080
FILING DATE: HERWITH
CLASSIFICATION NUMBER: PCT/US94/10080
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532
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/123,934
FILING DATE: 17-8EP-1993
CLASSIFICATION:
NAME: LAZAR, SLEVAN
NAME: LAZAR, SLEVAN
RECISTRATION NUMBER: 32,618
RECISTRATION NUMBER: 5203-PCT
TELECHONE: (617) 498-8260
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
TYPE: NUMBER: SINGle
TYPE: Nucleic acid
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2838.00
100.00%
100.00%
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// LOCATION: 61..1656
PCT-US94-10080-1
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CLONE: CFK1-23a
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Best Local Similarity:
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526
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Matches:
Conservative:
Mismatches:
               APPLICATION NUMBER: 9116099.2
APPLICATION NUMBER: 9116099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-600-645-2 (1-532) x US-09-382-256-13 (1-2070)
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SEQUENCE DESCRIPTION: SEQ ID
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2823.00
99.81%
98.87%
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                   internal
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                               421 HisPheGlnProTyrileMetAlaAspileTyrSerPheGlyLeuileIleTrpGluMet
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                                                                                                                                                                                                                                                                                 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg
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                                                        ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLy8Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOWAINS,
AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/02367
APPLICATION NUMBER: BCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: MAY 28, 1993
APPLICATION NUMBER: 9313763.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1621 Crcccaaagargerrgaarcccaggargraagarr 1656
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CORRESPONDENCE ADDRESS:
ADDRESSE: Fulbright & Jaworski L.L.)
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
RENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25
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Patent No. 6207814
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Pete:
FRANZEN, Petra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-382-256-13
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Sequence 13, Application US/09395115
Sequence 13, Application US/09395115
Sequence 13, Application US/09395115
Sequence 13, Application US/09395115
Sequence 13, Application:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik TITLE OF INVENTION: Activin Receptor-Like Kinase Domains And Their Use NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
   1777 CTTGCAAAATGGTTGAATCCCAGGATGTAAGATT 1812
                                                                                                                                                                                                                                                                                                                                           kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-NO. 6271365ember-1993
PRIOR APPLICATION NUMBER: 9224057.1
FILING DATE: 17-NO. 6271365ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                                                           inch, 360
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/395,115
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APPLICATION NUMBER: 9304680.3
FILING DATE: 8 - MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28 MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-UJY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-AUGUET-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 15-AUGUET-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-OCCODER-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOHIEİ, VİNEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: KOLLEI, VINEET
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 688-9200
TELEFAX: (212) 838-384
INPORMATION POR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                      STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: int
ORIGINAL SOURCE:
ORGANISM: Mouse
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                                   RESULT 5
US-09-395-115-13
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                                                                                         816
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; Sequence 13, Application US/08436265
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei, Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidecoshi; Heldin, Carl-Henrik; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their
          ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
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MEDIUM TYPE: Diskett
COMPUTER: IBM
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526
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILLING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION NUMBER: 9224057.1
FILLING DATE: 17-No. 6316217ember-1992
PRIOR APPLICATION NUMBER: 9304677.9
FILLING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILLING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 931047.6
FILLING DATE: 8-May-1993
PRIOR APPLICATION NUMBER: 9313763.6
FILLING DATE: 2-July-1993
PRIOR APPLICATION NUMBER: 9313763.6
FILLING DATE: 15-October-1993
PRIOR APPLICATION NUMBER: 9313744.5
FILLING DATE: 15-October-1993
PRIOR APPLICATION NUMBER: 9321344.5
FILLING DATE: 15-October-1993
PRIOR APPLICATION NUMBER: 9321344.5
FILLING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: 27,003
REFERENCE/DOCKET NUMBER: 100 5298
TELEPONNE: (212) 888-9200
TELEPONNICATION NUMBER: 21000
TELEPAN: (212) 888-9200
TELEPAN: (212) 888-9200
TELEPAN: CATON DATE: 2000 DASS PAIRS
LENGTH: 2000 DASS PAIRS
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2823.00
99.81%
98.87%
99.47%
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2070 base pair
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217..1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE: inte
ORIGINAL SOURCE:
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-436-265-13
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Mismatches:
Indels:
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Matches:
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                                  LUD 5298
            REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 668-9200
TELEPAX: (212) 838-388-
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2e-315
2823.00
99.81%
98.87%
                                                                                                                                                                                                                                                                                        internal
Kohlei, Vineet
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                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity:
                                                                                                                                                                                                                                               HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: i.
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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US-09-679-187-13
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DB:
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                                  1537 GCTCGTCGTTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATG 1596
                                                                                                                                                                                                                                                                    1717 TCAGAATGTTGGGCCCCATAATCCAGCCTCCAGACTCACAGCTTTGAGAATCAAGAAGAA 1776
                                                                                                                           1597 GIGCCCAGIGACCCATCCTATGAGACATGCGTGAGGTTGTGTGTGTGAAACGCTTGCGG 1656
                                                                                                                                                                                                       1657 ccaarcererraaccecregaacaeceareaarererregaecaerrrregaecraare 1716
                                                                                          480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                    ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg
                                                                                                                                                                                                                                             SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArglleLysLysThr
            AlaargargCys1leThrGlyGly1leValGluGluTyrGlnLeuProTyrTyrAsnMet
                                                                                                                                                                 481 ProlleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                              521 LeuAlaLysMetValGluSerGlnAspValLysile 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
CORRATING SYSTEM: PC-DOS
CONTAKENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-0CT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-0CCDBE-1995
FILING DATE: 17-NO. 6331621ember-1993
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-NO. 6331621ember-1993
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-NO. 6331621ember-1992
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION NUMBER: 9304680.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATE: 9313763.6
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-011y-1993
PRIOR APPLICATION DATE: 9136099.2
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09679187
Patent No. 6331621
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 932134.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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APPLICANT: MIYAZONO, Kohei
APPLICANT: IMAWIRA, Takeshe
APPLICANT: DEN DIJKE, Peter
TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE
FILE REPERBENCE: LUD 5339.1 CIP
CURRENT APPLICATION NUMBER: US/09/267,963D
CURRENT FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: US/09/30367
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1993-11-17
PRIOR FILING DATE: 1998-03-13
NUMBER: OF SEQ ID NOS: 46
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
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Matches:
Conservative:
Mismatches:
Indels:
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2823.00
99.81%
98.87%
99.47%
                                                                                                                                           TYPE: DNA
CORGANISM: Mus musculus
US-09-267-963D-13
                                                                                                                                                                                              Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                   LENGTH: 2070
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            CCAGTAGGAGAATCATTGAAAGACCTGATTGACCAGTCCCAAAGCTCTGGGGAGTGGATCT
                                                                     GlyLyeGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal
                                                                                                        LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr
                                                                                                                                          ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly
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 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer
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US-09-267-963D-13
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ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer

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Sequence 13, Application US/09267963D Patent No. 6692925 GENERAL INFORMATION:

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Receptor and a Type
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 Co-Transfected With a Type II BMP
BMP Receptor
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Mismatches:
Indels:
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MEDUM TYPE: Rloppy disk
COMPUTER: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,467B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hersko, Bart S.
REGISTRATION NUMBER: 32,572
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TITLE OF INVENTION: Co-Transfected With TITLE OF INVENTION: BMP Receptor WUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSE: The Procter & Gamble Compains STREET: 11810 East Miami River Road CITY: Ross STATE: OH
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 5474
TELECOMUNICATION INFORMATION:
TELEPHONE: (513) 627-0633
TELEFAX: (513) 627-0630
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2402 base pairs
TYRE: nucleic acid
STRANDENNESS: single
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2823.00
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Best Local Similarity:
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MOLECULE TYPE:
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Patent No. 6210899
GENERAL INFORMATION:
APPLICANT: Rosenbaum, Jan S
TITLE OF INVENTION: The Use of a BMP Protein Receptor
TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells
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                                  937 GGTAAAGGCCGCTATGGAGGAAGTATGGATAAATGGCGTGGTGAAAAAGTGGCTGTC
                                                                                                                                        LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr
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                GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal
                                                                           GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,735A
FILING DATE: 24.NOV-1993
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CORSTANJE, BRAHM J.
REFERENCE/DOCKET NUMBER: 5088
TELEPHONE: (513) 627-2858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BMP
                                                                                                                                                                                                      RESULT 10
US-08-158-735A-3
; Sequence 3, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:
; APPLICANT: COREA, PAUL E.
; APPLICANT: KOENIG, BETH B.
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: ROSENB
                                                                                       532
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Matches:
Conservative:
Mismatches:
                                                                                          LeuAlaLysMetValGluSerGlnAspValLysIle
                                                                                                                        US-10-600-645-2 (1-532) x US-08-158-735A-3 (1-2402)
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STREET: 11810 EAST MIAMI RIVER ROAD
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TOPOLOGY: linear
FEATURE:
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Best Local Similarity:
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                                    431 GTTGTTATAGGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTTGTGCTCTATTTCCATG
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   ValVallleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet
                                                                                                                                                      491 GCTGTCTGTATAGTTGCTATGATCATCTTCTCCCAGCTGCTTTTGCTATAAGCATTATTGT
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                                                                                   AlaArgArgCys1leThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet
                                                                                                                 1331 GCTCGTCGTTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATG
                      HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet
                                                                                                                                                            ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg
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Sequence 11, Application US/08334179A

Patent No. 6306625

GENERAL INFORMATION:

APPLICANT: ROSENBAUM, JAN S.

APPLICANT: NOHNO, TSUTOMU

APPLICANT: NOHNO, TSUTOMU

TITLE OF INVENTION: CON ENCODING A BMP TYPE II RECEPTOR

NUMBER OF SEQUENCES: 14
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATE:
APPLICATION DATE:
APPLICATION TOWN:
REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 5473
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-627-2858
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ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
STREET: 11810 EAST MIAMI RIVER ROAD
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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CITY: ROSS
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APPLICANT: CORREA, PAUL E.
APPLICANT: KOENIG, BETH B.
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: TING, JERRY
TITLE OF INVENTION: DNA SEQUENCE CODING FOR A FINDHER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER & GAMBLE COMPANY
STREET: 11810 EAST MIAMI RIVER ROAD
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COMPUTER: TBM PC COMPATIBLE
CONFUTER: TBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,735A
FILING DATE: 24-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08158735A
Patent No. 6248554
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ATTORNEY/AGENT INFORMATION:
NAME: CORSTANDE, BRAHM J.
REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 5088
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis
                                                                                                                                                                                          GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys
                                                                                                                                                                                                                                                             ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro
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                                                       US-10-600-645-2 (1-532) x US-08-334-179A-11 (1-2402)
  Mismatches:
Indels:
Gaps:
98.878
99.478
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 Local Similarity:
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                  LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys
                                                                                                                                  461 ValbroserAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg
                                                                                                                                                                                                                                                                         Sequence 5, Application US/08481337A
Patent No. 586373B
GENERAL INFORMATION:
APPLICANT: TEN DIJKE, Peter
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                                                                                    2056
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                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                             US-10-600-645-2 (1-532) x US-08-158-735A-1 (1-2056)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-2658
TELEFAX: (513) 627-2650
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2056 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
                                                                                    9.23e-313
2798.00
94.48%
93.59%
98.59%
                                                         CDS
join(291..1790)
                                                                                                Percent Similarity:
Best Local Similarity:
                                                             ;
US-08-158-735A-1
                                                         NAME/KEY:
                                                                               Alignment Scores:
Pred. No.:
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    ACAATAGAATGTTGTCGGACCAATTTATGTAACCAGTATTTGCAACCCACACTGCCCT
                                 ThrlleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro
                                                                                                                                                                                                                                                                GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550 CATTGCTTTGCCATCATAGAAGAAGATGACCAGGGAGAAACCACATTAGCTTCAGGGTGT
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohei
APPLICANT: SAMPATH, Kuber T.
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Worphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
STATE: MA
                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 310..1905
OTHER INFORMATION: /product= "Human ALK3"
                                                                                                                                                                                                                                                                                                                                                                                                                     3.68e-309
2769.00
98.50%
97.18%
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp
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Conservative:
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                  MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                LOCATION: 310..1905
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                 3.68e-309
                                                                                                                                                                                                                                                                                                    2769.00
98.50%
97.18%
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                                                                                                                                                               NAME/KEY: CDS
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Best Local Similarity:
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Pred. No.:
                                                                                                                                        FEATURE
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                                                            1750 CCAATTGTGTCTAATCGGGGAACAGTGATGATGTCTACGAGCAGTTTTGAAGCTAATG 1809
                                                                                                                                        501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArglleLysLysThr
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
FRANZEN, Petra
YANASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
AND THEIR USE
                                                                                                                                                                                                                       1870 CTTGCCAAGATGGTTGAATCCCAAGATGTAAAAATC 1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSILIALOW: 214
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: August: 91993
APPLICATION NUMBER: 9313763.6
FILING DATE: August: 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: August: 1993
APPLICATION NUMBER: 931344.5
FILING DATE: October 15, 1993
                                                                                                                                                                                                LeuAlaLysMetValGluSerGlnAspValLysile 532
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MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 318-3000
                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09382256A Patent No. 6207814 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5
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               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM
COMPUTER: MEDIUM SYSTEM: PC-DOS
SOFTWARE: Wordperfect
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Matches:
Conservative:
Mismatches:
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                                                                                                   SOFFWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/395,115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6271365ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-MARCH-1993
PRIOR APPLICATION DATA:
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NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERNICE/DOCKET NUMBER: LUD 5298
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRILOGATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION NUMBER: 931047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION NUMBER: 931047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION NUMBER: 931763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION NUMBER: 913609.2
FILING DATE: 3-AUGUEC-1993
PRIOR APPLICATION NUMBER: 913609.2
FILING DATE: 18-OCCODET-1993
ATTORNEY/AGRET INCORMATION:
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2769.00
98.50%
97.18%
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TYPE: nucleic acid
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STRANDEDNESS:
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                                                                                                                                                  1270 CTGAAATGTGCTACACTGGACACCAGAGCCCTGCTTAAATTGGCTTATTCAGCTGCCTGT 1329
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Sequence 5, Application US/09395115
Patent No. 6271365
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Activin Receptor-Like Kinase Domains And Their Use NUMBER OF SEQUENCES: 29
CORRESPONDENCE 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
CITY: New York City
STATE: New York City
                                                                                                                        ValleuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
                                                                                                                                                                                                          SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
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                                      261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr
                                                                  1090 AAAGTATTCTTTACCACTGAAGAAGCCAGCTGGTTTCGAGAAAACAGAAATCTACCAAACT
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APPLICANT: Lin, Herbert Y.
APPLICANT: Mang, Xiao-Fan
APPLICANT: Weinberg, Xiao-Fan
APPLICANT: Weinberg, Xiao-Fan
APPLICANT: Weinberg, Robert A.
APPLICANT: Lodish, Harvey F.
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-LOOPCLE - LOOPEXTE - UNITS=bite -START=1 -END=-1.MATRIX=blosum62
-LOOPCLE - LOOPEXTE - UNITS=bite -START=1 -END=-1.MATRIX=blosum62
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEDF=0 -XGAPEXT=0.5
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                                                                                                                              TGCATGAGCAACTGC -----AGCATCACCTCCATCTGTGAGAAGCCACAGGAAGTC
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                    Matches:
Conservative:
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Indels:
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        3.52e-55
561.50
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29.15%
                                                                                   US-10-600-645-2 (1-532)
                               Percent Similarity:
Best Local Similarity:
Alignment Scores:
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APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATINC
TITLE OF INVENTION: CANCERS
FILE REPERENCE: AM10.1079 (0.31896-01.0000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PatentIn version 3.2
SEQ ID NO 35
LENGTH: 35.27
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| GAAGTCCTAGAATCCAGGATGAAATTGCTGAGTCCTTCAAGCAGACCGATGTC 1676
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                                       GlnGlyLysPro----AlaileAlaHisArgAspLeuLysSerLysAsnIleLeuIle
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Conservative:
Mismatches:
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Best Local Similarity:
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US-10-770-726-35
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APPLICANT: Raju, Jeyasealan
TITLE OF INVENTION: NOVEL CARK PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MI-068CP2
CURRENT APPLICATION NUMBER: US/11/186,283
CURRENT PILING DATE: 2005-07-21
PRIOR PILING DATE: 2005-07-24
PRIOR PELICATION NUMBER: US/09/947,199A
PRIOR PILING DATE: 2001-09-05
PRIOR PELICATION NUMBER: US/09/947,199A
PRIOR PILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 09/291,839
PRIOR APPLICATION NUMBER: US 09/291,839
PRIOR APPLICATION NUMBER: US 09/291,839
PRIOR APPLICATION NUMBER: US 09/291,839
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PRIOR APPLICATION NUMBER: US 09/291,839
PRIOR APPLICATION NUMBER: US 09/291,839
PRIOR APPLICATION NUMBER: US 09/291,839
PRIOR PILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ 1D NOS: 9
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Matches:
                     Sequence 3, Application US/11186283 Publication No. US20050255520A1 GENERAL INFORMATION:
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1408 TCCGGCTACTTTGGGGAGTCTTCGAGGGGCTCTGGAAAGACCGGGTCCAGGTGGCCATT 1467
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1468 AAGGTGATT--------TCTCGAGACAACCTCCTGCACCAG 1503
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197 GluAlaPhelleProValGlyGluSerLeuLy8AspLeuIleAspGlnSerGlnSerSer 216
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; LOCATION: (48)..(2552)
US-11-186-283-1
                                                                         Alignment Scores:
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Publication No. US2005025520A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL CARK PROTEIN AND NUCLEIC ACID MOLECULES AND USES

TITLE OF INVENTION: NOVEL CARK PROTEIN AND NUCLEIC ACID MOLECULES AND USES

TITLE OF INVENTION: NOVER.

FILE REFERENCE: MNI-06867P2

CURRENT APPLICATION NUMBER: US/11/186,283

CURRENT APPLICATION NUMBER: US/09/947,199A

PRIOR FILING DATE: 2003-07-21

PRIOR PELING DATE: 2001-09-05

PRIOR PELING DATE: 2001-09-05

PRIOR PELING DATE: 1999-12-11

PRIOR FILING DATE: 1999-12-11

PRIOR FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PALENTIN NUMBER: US 09/458,457

PRIOR FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 9

SEQ ID NO 1

LENGTH DATE: DATE OF THE OFFICE OF
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1807 GTGGTGGCAGATTTTGGAGAATCA---AGATTTCTACAGTCTCTGGATGAAGACAAC--- 1860
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1963 CTGTGGGAAATF------CTCACTGGC-------GAAATTCCA 1992
                                        ---ATGACAAAACAACCTGGGAACCTCGGTTGGATGGCTGTGAGGTGTTCACGCAGTGC 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1993 TICGCICATCICAAGCCAGCGGCTGCGCAGCAGACATGGCTTACCACCACATCAGACCT 2052
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                                                                                                                                                                                357 AlaileAlaHisArgAspLeuLysSerLysAsnileLeulleLysLysAsnGlySerCys 376
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                                                                                              337 SerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysPro 356
                                                                                                                                                                                                                                                                                                                                                                        397 ProLeuAsnThrArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSer 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457 TyrTyrAsnMetValPro-----SerAspProSerTyrGluAspMetArgGlu 472
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         319 AspPheLeu-----LysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyr 336
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                                                                                                                        2170 TGCAACATTGAGCTGATGTCTCCTGCATCA 2199
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ORGANISM: Homo sapiens
FEATURE:
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1410 CATTICCATCTICAGCICTCA--GAAATIGAGTICCATGAGATTATIGGCTCAGGTICT 1466
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1692 TCCCTCCTTCATGAGCAGAGAGAGATTCTTGCAGTTTGCAGTTAATTATTGCAGTA 1751
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                                                                                                                                                                                                                        LysHisTyr------CysLysSerIleSerSerArgGlyArg 188
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    3025
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132
74
21
                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                        US-10-600-645-2 (1-532) x US-11-186-283-1 (1-3025)
       Length:
Matches:
6.2e-18
248.00
44.32%
25.95%
8.74%
                                                    Percent Similarity:
Best Local Similarity:
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84 AlaileileGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCysMet	Db 1029 ATTGCACTCTGCTTGCTACCA	265 ThrThrGluGlualaSerTrpheArgGluThrGluIleTyrGlnThrValLeuMet :::1495 TCCAAGTCAGACGGGATATTTTCCCGAGAGGTCCATTCTCTGCCAGCTC :::1549 AACACCCCTGCGTGGTTCAGTTTGTGGGTGCCTGCTTGCATTCTCTGCCAGCTC :::1549 AACCACCCCTGGTTCAGTTTGTGGGTGCCTGCTTGGATGACCCCAGT ::::1
Qy 457 TyrTyrAsnMetValProSerAspProSerTyrGluAspMetArgGlu 472 1:::	RESULT 5 US-11-186-283-9 Sequence 9, Application US/11186283 Sequence 9, Application W1/11186283 Publication No. US200505552041 GENERAL INFORMATION: APPLICANT: Raiu, Jeyaseelan TITLE OF INVENTION: APPLICANT: Raiu, Jeyaseelan TITLE OF INVENTION: TITLE OF INVENTION: FILE OF INVENTION: FURENT APPLICATION UNDER: US/11/186,283 CURRENT APPLICATION NUMBER: US/0520,173 PRIOR FILING DATE: 2005-07-21 PRIOR APPLICATION NUMBER: US/09/947,199A PRIOR FILING DATE: 1999-04-14 PRIOR APPLICATION NUMBER: US/09/947,199A PRIOR APPLICATION NUMBER: US/09/947,199A PRIOR APPLICATION NUMBER: US/09/111,038 PRIOR FILING DATE: 1999-04-14 PRIOR APPLICATION NUMBER: US/09/111,038 PRIOR FILING DATE: 1999-04-14 PRIOR APPLICATION NUMBER: US/09/111,038 PRIOR FILING DATE: 1999-112-10 NUMBER OF SEQ ID NOS: 9 SEQ ID NOS: 9 SEQ ID NO 9 SEQ ID NA ORGANISM: Rattus norvegicus FEATURE: NAMB/REY CDS LOCATION: (1)(2505) US-11-186-283-9	Alignment Scores: 2.34e-17

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Publication No. US2005025520A1

GENERAL INFORMATION:

APPLICANT: Raju, Jeyaseelan

TITLE OF INVENTION: WOVEL CARK PROTEIN AND NUCLEIC ACID MOLECULES AND USES

TITLE OF INVENTION: THEREFOR

FILE REPERBRUE: MI-068CP2

CURRENT APPLICATION NUMBER: US/11/186,283

CURRENT APPLICATION NUMBER: US/10/626,173

PRIOR APPLICATION NUMBER: US/09/947,199A

PRIOR APPLICATION NUMBER: US 60/111,938

PRIOR APPLICATION NUMBER: US 60/111,938

PRIOR APPLICATION NUMBER: US 09/291,839

PRIOR APPLICATION NUMBER: US 09/291,839

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

LENGTH: 3026
                 |||| ::: :::|||
|GAGAATCA----AGATTTCTGCAGTCCCTGGATGAAGACAAC-----ATGACAAAGCAG 1872
                                                                      1873 CCAGGGAACCTGCGCTGGATGCCCCTGAGGTGTTCACACAGTGCACGAGATACACC--- 1929
                                                                                                                1975 ------CTCACTGGA-------GAAATTCCATTCGCTCATCTCAAG 2007
                                                                                                                                                                                                                    2008 CCAGCCGCTGCAGCAGCAGTATGGCGTATCACCACATCAGACCGCCCATCGGCTATTCC 2067
                                                                                                                                                                                                                                                                                                                        2128 CCAGAGTTCTCTGAAGTCGTTAGCAAACTGGAGGAGGGCCTATGCAATGTG---GAGCTC 2184
                                                                                                                                                                                                                                                                      422 PheGlnProTyrileMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMetAla 441
                                                402 ValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsnHis 421
                                                                                                                                                                                                  462 Pro------SerAspProSerTyrGluAspMetArgGluValValCysValLys 477
GlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThrArg 401
                                                                                                                                                 442 ArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMetVal
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Mismatches:
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Matches:
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ORGANISM: Rattus norvegicus
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40.44%
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; LOCATION: (61)..(2565)
US-11-186-283-7
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Query Match:
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US-10-600-645-2 (1-532) x US-11-186-283-7 (1-3026)

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969 CTTCAGCGAGACATTTCACAGTGCTTGTACCTATGGCAAGAACATTGACCTGGTCAA 1028
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435 CAACTCTCCGAAATCGAGTTCCACGAGATTATCGGCTCGGGTTCCTTTGGGAAAGTCTAT 1494
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| AACATTGTGAAACTCCTGGTAGAAGAAGGAGCAAAGCAGATGTGAACGCTCAG----- 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       910 GAAGTTGCCAAGGAAATTGTCCAGGTAACAGGAACTGAAAGTCTGACTAA-GGAAAACAT 968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 PheAspGlySerValArgTrpLeuAlaValLeuIleSerMetAlaValCysIleValAla 166
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                                                                                                                                                                                                                                                                                                                                796 GGACACCACAATATAGTGAGCTACCTGCTCCAGAGTGACTTAGAGGTCCAGCCTCACGTC 855
AsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAspGlnLysLysPro 44
                                                                                                                                                                                                  -------GAAGACCACGTCCCTCTGCACTTCTGTTCTCATTT
                                                                                                                             GluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 ThrileAlaLysGlnileGlnMetValArgGlnValGlyLysGlyArgTyrGlyGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2059 TACAAGGCCATGCTGAAGACATCCTCGGGAAGAAGGAGGTGCCGGTGGCCATCAAGACG
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                         OTHER INFORMATION: Fusion protein coding sequence
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    PRIOR APPLICATION NUMBER: US 60/556,744
RIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                         ORGANISM: Artificial Seguence
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41.96%
24.37%
8.51%
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                                                                                                   SEQ ID NO 3
LENGTH: 3105
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Sequence 3, Application US/11021441

Publication No. US20050249748A1

GENERAL INFORMATION:

APPLICANT: DUBENSKY, Thomas W., Jr.

APPLICANT: DORTNOY, Daniel A.,

APPLICANT: COOK, David N., Jr.

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE

TITLE OF INVENTION: THEREOF

FILE OF INVENTION: THEREOF

FILE OF INVENTION NUMBER: US/11/021,441

CURRENT APPLICATION NUMBER: US 60/615,750

PRIOR APPLICATION NUMBER: US 60/615,287

PRIOR FILING DATE: 2004-10-01

PRIOR FILING DATE: 2004-01-00-01

PRIOR FILING DATE: 2004-08-05

PRIOR FILING DATE: 2004-08-05

PRIOR FILING DATE: 2004-07-07-23

PRIOR FILING DATE: 2004-07-07-33

PRIOR FILING DATE: 2004-06-30
                             1933 CCAGGGAACCTGCGCTGGATGGCCCCTGAGGTGTTCACAGTGCACGAGATACACC--- 1989
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GlnLeuTyrLeulleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeu-----
                                                                                                                            LeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHisArg
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                                                                                                 LysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGly
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; Sequence 4, Application US/10990276; Publication No. US20050255549A1; GENERAL INFORMATION:
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APPLICANT: Li, Shyun
APPLICANT: Li, Shyun
APPLICANT: Li, Shyun
APPLICANT: Li, Shyun
APPLICANT: Li, Shyun
ATTLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US/09/759,595
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
LENGTH: 1383
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Conservative:
Mismatches:
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Publication No. US20050255549A1
GENERAL INFORMATION:
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OTHER INFORMATION: human IRAK-4
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ORGANISM: Homo sapiens
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Score:
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                                           PhelleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAsp 310
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691 gatcaagaataaagtaatggcaagtgtcaacatgaaacttagtagaactacttggt
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APPLICANT: Li, Shyun
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
TITLE OP INVENTION: IRAC.4: Compositions and Methods of
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/10/990,276
CURRENT FILING DATE: 2004-11-15
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OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
OTHER INFORMATION: CDNA
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Matches:
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PRIOR APPLICATION NUMBER: US/09/759,595
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 4
: LENGTH: 1542
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COCATION: (1542)
COTHER INFORMATION: murine IRAK-4
US-10-990-276-4
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Best Local Similarity:
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                                                                                                                             TYPE: DNA ORGANISM: Mus sp.
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S G	Qy 379 AlaAspLeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeu :::	eProLeu 398 ::: GGTCATG 1194
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8 8	418	
ΩD		GGTTCTG 1293
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USS COLOR OF THE C	ESULT 10 S-10-770-726-17 S-10-770-726-17 Sequence 17, Application US/10770726 Publication No. US20050266409A1 GENERAL INFORMATION: APPLICANT: Weth APPLICANT: Brown, Eugene APPLICANT: Liu, Weth TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, TITLE OF INVENTION: CANCERS. FILE REFERENCE: AM101079 (031896-010000) CURRENT APPLICATION NUMBER: US/10/770,726 CURRENT FILING DATE: 2004-02-04 NUMBER OF SEQ ID NOS: 48640 SOFTWARE: Patentin version 3.2 SEQ ID NO 17 LENGTH: 6058 TYPE: DNA ORGANISM: Homo sapiens	PREVENTING, AND TREATIN
Ali Sco Sco Per Bes Oue	Alignment Scores: 7.37e-15 Length: 6058 Score: 226.00 Matches: 99 Percent Similarity: 40.80% Conservative: 74 Percent Similarity: 23.35% Mismatches: 137 Query Match: 6 Gaps: 21	
ns.	US-10-600-645-2 (1-532) x US-10-770-726-17 (1-6058)	
SP GS	Qy 140 ProValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIl	IlleSer 159 ::: CGTCATC 1701
ò	Qy 160 MetAlaValCyBIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyr	HisTyr 179
д	Db 1702 GCCATCGTGTGT	1713
ò	180 C	Phe 19
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ò	200 IleProValGlyGluSerLeuLy	erG1y
අු	Db 1747CAGTACACGGACAAGCTGCAACACCTGCAACACCTACAGGTGG	AGTGGC 1782
ò	22	227
gn	1783	8
ço da	Oy 228ArgThrIlealaLysGlnIleGlnMetValargGlnVal	Val 240 GTGATC 1902
ò	Oy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLys	Lys 257 :::

us-10-600-645-2.rnpbn

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CysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAsp 362
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                        258 -----ValAlaValLysValPhe-----PheThrThrGluGluAlaSerTrpPhe 272
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Publication No. US20050249748A1
Publication No. US20050249748A1
Publication No. US20050249748A1
APPLICANT: INFORMATION:
APPLICANT: LOUERTY, William S., Jr.
APPLICANT: COOK, David N.
TITLE OF INVENTION: EXPRESSION CASSETTES, AND METHODS OF
                                                                                                                                                                                       484 SerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCys
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                                                                       273 ArgGluThrGluIleTyrGlnThrValLeuMet-----ArgHisGluAsnIleLeu
                                                                                                                       290 GlyPhelleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThr
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ATGATGATCATCACTGAGTACATGGAGAATGGGGCCCTGGACAAGTTCCTTCGGGAGAAG 630
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; OTHER INFORMATION: Fusion protein coding sequence
WS-11-021-441-19
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Matches:
Conservative:
Mismatches:
Indels:
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FILE REFERENCE: 282172003900
CURRENT APPLICATION NUMBER: US/11/021,441
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: US 60/616,750
PRIOR FILING DATE: 2004-10-06
PRIOR FILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-06-05
PRIOR FILING DATE: 2004-06-05
PRIOR FILING DATE: 2004-06-05
PRIOR FILING DATE: 2004-06-05
PRIOR FILING DATE: 2004-07-23
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
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ignment Scores: ed. No.:	Oy 186 ArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheileProValGly 203	221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 24 124 GCTGTGTTGAAGTTCACTACCGAGATCCATCCTCTGTCACTCGGCAGAAGGTGATC 18 241 GlyLysGlyArgTyrGlyGlUValTrpMetGlyLysTrpArgGlyGluLysVa. 25	DD 184 GGAGCAGGAGAGTTTGGGGAGGTGTACAAGGCCATGCTGAAGACATCCTCGGGGAAGAAG 243 Qy 259 AlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTy: 278	Db 295 GGAGTGGACTTCCTCGGCGAGGCCGGCATCATCAGCCACCACACATCATC 354 Qy 295 AsplleLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGlu 313 Db 355 GGCCTAGAGGGGTCATCTCCCAAATACAAGGCCCATGATGATGATGATCATGAGAG 414	Qy 314 AsnGlySerLeufyrAspPheleuLysCysAlarhrLeuAspThrAspAlaleu 331 415 AAGGGCCCGGACAGAAGGTGCGAGAGGTGCGCGTGCTGCTGCTG 74 Db 415 AATGGGCCCTGGACAGTTCTTCGGGAGAGGTGGCGAGTTCAGCGTGCTGCTGCTG 74 Qy 332 LeuLysLeuAlaTyrSerAlaAlaCyGGLTGCTGGCCTGCCCGCAACATGACTAT 531 Qy 352 ThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsmIleLeuIleLys 371 Db 532
	Qy 397 ProLeuAsnThrArgYalGlyThrArgArgTyrMetAlaProGluValLeuAspGluSer 416	436 IlelleTrpGluMetAlaArgArgCyslleThrGlyGlylleValGluGluTyrGlnLeu :::::	BArgleuArgProl	Db 1042 GCCATCTACCAGGTCATGATGCAGCAGCAGCAGCAGCGCGCCCCCAAGTTC 1101 Qy 515 LeuargileLysThrLeualaLysMetValGluSerGlnAsp 529 Db 1102 GCTGACATCGTCAGCATCCTCGACACACTTCGTGCCCTGAC 1146	RESULT 12 US-11-021-441-16 US-11-021-441-16 US-11-021-441-16 US-11-021-441-16 US-11-021-441-16 EQUIDIDATION NO. USZO050249748A1 GENERAL INFORMATION: APPLICANT: DORINGY, Thomas W., Jr. APPLICANT: DORINGY, Daniel A. TITLE OF INVENTION: EXCOMENIANT NUCLEIC ACID MOLECULES, TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: THEREOF TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, FILE REFERENCE: 2021-203 FORTOR FILING DATE: 2004-10-01 FRIOR PILING DATE: 2004-00-05 FRIOR FILING DATE: 2004-00-05 FRIOR PILING DATE: 2004-00-32 FRIOR FILING DATE: 2004-03-36 NUMBER OF SEQ ID NOS: 129 SPRIOR FILING DATE: 2004-03-36 NUMBER OF SEQ ID NOS: 129 SPRIOR FILING DATE: 2004-03-36 NUMBER OF SEQ ID NOS: 129 SPRIOR FILING DATE: 2004-03-36 NUMBER OF SEQ ID NOS: 129 SPRIOR FILING DATE: 2004-03-36 NUMBER OF SEQ ID NOS: 129 SPRIOR FILING DATE: 2004-03-36 NUMBER OF SEQ ID NOS: 129 SPRIOR FILING DATE: 2004-03-36 NUMBER OF SEQ ID NOS: 129 SPRIOR PLING WATER APPLICATION NUMBER: PARTING WATER APPLICA

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GlyLysGlyArgTyrGlyGluValTrpMetGly-----LysTrpArgGlyGluLysVal 258
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373 AATGATGCAATGTTGGCAACAAGAAAGAGCACGACGTCCAAAATTTGCAGATATTGTTAG 932
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709 ACAAGTGCATCAGACGTGTGGAGTTTTGGGATTGTAATGTGGGAAGTT-----
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Publication No. US20050249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: PORTNOY, Daniel A.
APPLICANT: LUCKETT, William S., Jr.
APPLICANT: COOK, David N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 ArgGlyArgTyrAsnArgAspLeuGluGln-----AspGluAlaPheIleProValGly 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluSerLeuLysAspLeu-----IleAspGlnSerGlnSerSerGlySerGlySer 220
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                                                                                       -----GACTGCCCTCCGCCATCTACCAGCTCATGATGCAGTGC
                                                                                                                                  504 TrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                      Sequence 17. Application US/11021441

Bublication No. US20050249748A1

GENERAL INFORMATION:
APPLICANT: DUBRENKY, Thomas W., Jr.
APPLICANT: DUBRENKY, Thomas W., Jr.
APPLICANT: LUCKETT, William S., Jr.
APPLICANT: COOK, David N.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: REPRESSION CASSETTES, AND BACTERIA, AND
TITLE OF INVENTION: BERRESSION CASSETTES, AND BACTERIA, COOK, INVENTION: BERRESSION CASSETTES, AND BACTERIA, NUCRENT OF INVENTION: THEREOF
FILE REFERENCE: 282172003900
CURRENT FILING DATE: 2004-12-23
PRIOR PLILOR DATE: 2004-10-01
PRIOR PLILOR DATE: 2004-10-01
PRIOR PLILOR DATE: 2004-00-01
PRIOR PLILOR DATE: 2004-00-01
PRIOR PLILOR DATE: 2004-00-03
PRIOR PLILOR DATE: 2004-00-30
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                          524 MetValGluSerGlnAsp 529
                                                                                                                                                                                                                                                           946 CTCATTCGTGCCCTGAC 963
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Best Local Similari
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sequence 25, Application US/11021441
sequence 25, Application US/11021441
sequence 25, Application No. US20050249748A1
sequence 25, Application No. US20050249748A1
sembla in Pornation No. US20050249748A1
septication No. US20050249748A1
septication UCKETY, William S., Jr.
APPLICANT: DUCKETY, William S., Jr.
APPLICANT: CONCK, David N.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: PERRESSION CASSETTES, AND BACTERIA, AND METHODS OF USF
TITLE OF INVENTION: THEREOF
FILE REPRENCE: 282172003900
CURRENT APPLICATION NUMBER: US 60/616, 750
PRIOR APPLICATION NUMBER: US 60/615, 287
PRIOR APPLICATION NUMBER: US 60/615, 287
PRIOR FILING DATE: 2004-10-01
PRIOR PELING DATE: 2004-01-0-05
PRIOR APPLICATION NUMBER: US 60/559, 377
PRIOR APPLICATION NUMBER: US 60/556, 744
PRIOR PELING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: US 60/556, 744
PRIOR PELING DATE: 2004-07-26
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 25
LENGTH: 1716
                                                                                                                                                                                                                                                                                                                                                                                                  1054 CGTTGGACAGCACCGGAAGCAATTTCA--------TATCGTAAATT7' 1092
                                                                                                                                                                                              1270 TGGCAACAAGAAGAGCTAGAAGACCTAAATTTGCAGACATTGTTCAATTTTAGACAAA 1329
                                                                                                                                                                                                                                                                                                                                                         ArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTyr 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                        | IleThrGlyGly1leValGluGluTyrGlnLeuProTyrTyrAsnMetValProSerAsp 464
                    859 GTTGGTATGTTACGTGGCATCGCTGCAGGTATGAAATATCTTGCCAACATGAATTAT--- 915
                                                               352 ThrGlnGlyLysProAlalleAlaHisArgAspLeuLysSerLysAsnIleLeuIleLys 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504 TrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArglleLysLysThrLeuAlaLys 523
                                                                                                                                                                                                                                                              ----ThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArg
                                                                                                               ---GTACATAGAGATTTAGGGGCTCGAAATATTCTTGTAAAT
                                                                                                                                                                372 LysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLysPheAsnSerAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 ProSerTyrGluAspMetArgGluValValCysValLysArgLeu---ArgProlleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484 SerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCys
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TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 282172003900
CURRENT FILING DATE: 2004-12-23
FRICH APPLICATION NUMBER: US 60/616,750
PRIOR PLILING DATE: 2004-10-06
PRIOR PLILING DATE: 2004-10-06
PRIOR FILING DATE: 2004-10-01
PRIOR FILING DATE: 2004-0-0-05
PRIOR FILING DATE: 2004-0-0-05
PRIOR FILING DATE: 2004-0-0-05
PRIOR FILING DATE: 2004-0-0-05
PRIOR PLICATION NUMBER: US 10/683,599
PRIOR FILING DATE: 2004-0-0-26
PRIOR PLILOR DATE: 2004-0-0-26
PRIOR PELICATION NUMBER: US 10/683,599
PRIOR PLILING DATE: 2004-0-0-26
PRIOR PELICATION NUMBER: US 10/683,599
PRIOR PLILING DATE: 2004-0-0-26
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PRIOR PELICATION NUMBER: US 10/683,599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 GCGGTCCTTAAATTTACAACCGAAATTCATCCATCATGCGTAACTCGTCAAAAAGTGATC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GlyLysGlyArgTyrGlyGluValTrpMetGly-----LysTrpArgGlyGluLysVal 258
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GGAGCTGGAGAATTCGGGGAGGTATACAAAGGCATGTTGAAAAACCTCAAGTGGTAAAAAA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AlavaliysvalPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyr 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAla------Ala 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 ArgGlyArgTyrAsnArgAspLeuGluGln-----AspGluAlaPheIleProValGly 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnGlySerLeuTyrAspPheLeu-----LysCysAlaThrLeuAspThrArgAlaLeu 331
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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LENGTH: 1382
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                                                                                                                                                                                                                                                                                              486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyLysGlyArgTyrGlyGluValTrpMetGly-----LysTrpArgGlyGluLysVal 258
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                                                                                                                                                                                                                                                              186 ArgGlyArgTyrAsnArgAspLeuGluGln-----AspGluAlaPheIleProValGly 203
                                                                                                                                                                                                                                                                                                                                                           GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
                                                                                                                                                                                                                                                                                                                                                                                                                           547 GCAGTATTAAAATTTACAACAGAAATACACCCAAGTTGTGTTACAAGACAAAAAGTTATT 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 GlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAla------Ala 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           718 CGAGTTGATTTTTTAGGTGAAGCAGGAATTATGGGTCAATTTAGCCATCATAATATTATT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 AspileLysGlyThr -- GlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGlu 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        838 AACGGIGCTTTAGATAAATTTTTACGIGAAAAGGAIGGIGAAITTTAGIGTTTIACAATTG 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 ThrGlnGlyLysProAlalleAlaHisArgAspLeuLysSerLysAsnIleLeuIleLys 371
                                                                                                                                                                                                                                                                                ||| || || || || || || AGACGTGCTCGACAATCCCCAGAAGATGTGTTTTTCGAAAGT
                                             OTHER INFORMATION: Expression cassette, encodes fusion protein
                                                                                                            1716
94
59
141
78
                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                            US-10-600-645-2 (1-532) x US-11-021-441-25 (1-1716)
TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                          2.94e-15
222.00
41.24%
25.34%
                                                                                                                                                          Best Local Similarity:
Query Match:
DB:
                                                                                                                                              Percent Similarity:
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Pred. No.:
                                                  ; OTHER INFORMA
US-11-021-441-25
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|296 AATGATGCAATGTTGGCAACAAGAAAGAGCACGACGTCCCAAAATTTGCAGATATTGTTAG 1355
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                                                                                              Asn---ArgTrp----AsnSerAsp-GluCysLeuArgAlaValLeuLysLe
                                         ProSerTyrGluAspMetArgGluValValCysValLysArgLeuArgProIleValSer
                                                                                                                                                   499 uMetSerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLy
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1180 ATGACATATGGA
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Search completed: December 10, 2005, 00:13:01 Job time : 183 secs

Run

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CK638737 UI-M-H00-CK638737 UI-M-H00-CP744610 UI-M-H00-CD24444 AGENCOURT BI767125 JGI CAB19 CM50811 UI-M-H20-CD35147 UI-M-H20-CD352147 UI-M-H20-CD35214 UI-M-GI0-CD35214 UI-M-GI0-CD35214 UI-M-H20-CD35214 UI-M-H00-CM57338 UI-M-H00-CM57338 UI-M-H00-CM573314 UI-M-H30-CM57314 UI-M-H30-CM558110 UI-M-H20-CM57314 UI-M-H20-CM558110 UI-M-H20-
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AY417400 Pan trog1
AX653428 Mus muscu
AY417401 Mus muscu
CD352073 UI-M-GI0-
CK965863 4080965 B
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Mus musculus BMPRIA gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 1521)
1 (bases 1 to 1521)
1 cdd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, White, T.J., Sninsky, J.J.,
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1521)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
         AU124197
DR156725
CX204646
CK638737
CF744610
AU124052
CV557698
CC0544444
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           AU124197
CX2048737
CX2048137
CY538737
CY546610
AU124052
CV557698
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CY557698
CY63937
CN643937
CN643937
CN643937
CN643933
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CV55490
AU125490
AU125490
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CK965863
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AY411158.1 GI:39767126
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AY411158
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-MODEL-frame+ plan.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US10600645/runat_02122005_103605_23292/app_query.fasta_1.711
-Q=/cgn2_1/USPTO_spool/US10600645/runat_02122005_103605_23292/app_query.fasta_1.711
-DB-EST -QPMT=fastap -SUFFTX=rst - MINMATCH=0.1 -LOOPCL=0 - LOOPEXT=0
-UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10600645_GCGN 1 1 4015_GNINLEN=0 -MAXLEN=200000000
-USER-US10600645_GCGN 1 1 4015_GNINT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPORT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AY411156 Homo sapi
AY411157 Pan trogl
AK086130 Mus muscu
AY418113 Homo sapi
AY418115 Mus muscu
AY418114 Pan trogl
                                                                                      2005, 19:17:20 ; Search time 4008 Seconds (without alignments) 6210.261 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                             US-10-600-645-2
2838
1 MTQLYTXIRLLGACLFIISH......TALRIKKTLAKMVESQDVKI
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                    41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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AY418115
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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gb_est6:*
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1532 bp DNA linear GSS 16-DEC-2003
Homo sapiens BMPR1A gene, VIRTUAL TRANSCRIPT, partial sequence,
Avail1156
SAVA11156.1 GI:39767124
GSS.
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                                                                                AlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCys 343
                                                             902
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I (base 1 to 1532)

Clark, A.G. (Janowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Territera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, Wholey to the control of the connectral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                        CACCTCCACAGAAATTTATGGTACCCAAGGGAAGCCTGCAATTGCTCATCGAGACCTG
   AlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThrArgValGly
                                                                                                                                                                                                                                              ThrargargTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGln
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AY411156
LOCUS
DEFINITION
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1. 1521
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/db_xref="taxon:10090"
<1._>1521
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Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                          723 TTTACCACTGAAGAAGCCAGCTGGTTTCGAGAAACAGAAATCTACCAAACTGTGCTAATG
                                                                                                          GlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeuLysCys
                                                                                                                                                                  CAGCTCTATTTGATTACTGATTACCATGAAAATGGATCTCTCTATGACTTCCTGAAATGT
                                                                                                                                                                                                                                                      963 CACCTGCACACAGAATTTATGGCACCCAAGGAAAGCCCGCAATTGCTCATCGAGACCTA
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                                                              PheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMet
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      Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A. Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A. Todanowski, S., Nielson, C., Lu, F., Murphy, B., Adams, M.D. and Cargill, M. Diect Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and orderithem based on alignment.
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Matches:
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                                                                                                                    Location/Qualifiers
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98.04%
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 ATTGATAACATGCTCTTACGAAGCTCTGGAAATTAAATGTGGGCACCAAGAAG---GAG 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 AsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCysSerGly 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HisCysProAspAspAlalleAsnAsnThrCysIleThrAsnGlyHisCysPheAlalle 85
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prepare mouse tibbuce.
Please visit our web site for fu
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                AKO86130 mRNA linear HTC 03-APR-2004 was musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930007102 product:bone morphogenetic protein receptor, type 1B, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Zakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Murametsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Analysis of the mouse transcriptome based on functional annotation
6.60,770 (111-length cDNAs
Nature 420, 563-573 (2002)
6. (bases 1 to 1911)
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Glires; Rodentia;
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cagtgtcgggacactccccattcctcatcaagaagatcaattgaatgctgcacagaaagg 297
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                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
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BMPRIB gene, VIRTUAL TRANSCRIPT, partial sequence
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GCTGACATGTACAGCTTTGGACTCATCCTCTGGGAGATTGCAAGGAGATGTGTTTCTGGA 125:
                                                                                                                                                                                                                                                                             1509 bp DNA linear GSS 17-DEC-200 genetroglodytes BMPR1B gene, VIRTUAL TRANSCRIPT, partial sequence, AY418114
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, 10 monindae, Pan. (Dases 1 to 1509) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaun,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD. 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                      AsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCysTrpAlaHisAsn
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Mismatches:
Indels:
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Query Match:
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| CAATGTCGTGACACTCCCATTCCTCATCAAAGAAGATCAATTGAATGCTGCACAGAAAGG
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                   Aricititiccaagtccagaaaattaaatcrcccaccaaaaa---caacatccrcac
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|GATACAGCATTGGGTTAGAACAGGATGAAACTTACATTCCTCCTGGAGAATCCTGAGA
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/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="rMAGE:5562094"
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/done_lib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site=1: NOTI; Site=2: Sall; Cloned unidirectionally;
oligo-dT primed Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
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AGENCOURT 6466656 NIH_MGC_88 Homo sapiens cDNA clone IMACE:5562094
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 1121)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12290 row: o column: 23
High quality sequence stop: 679.
Location/Qualifiers
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us-10-600-645-2.rst

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Hall human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Sugano,S., Isogai,T.)

Lupublished (2000)

Contact: Takao Isogai
Genomics Laboratory
Hellx Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3975
Fax: 81-438-52-3976
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institutes
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="NT2RM2"
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precursor cells"
                                                                                                                                                                                                                  mRNA linear EST 01-AUG-2002
clone NT2RM2001814 5', mRNA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 874)
Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                   TCCAGCTGGCCTGGGGCCACCTGCCCCCAGAAATTTATGGGCCCCCAAGAAAAG
356 --ProAlaIleAlaHisArgAspLeuLysSerLysAsnIleLeulle-LysLysAsn-Gl
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                  AU124197 AU124197 NT2RM2 Homo sapiens cDNA
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AU124197.1 GI:10948913
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96.54%
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Homo sapiens
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 rechnologies. Note: this is a NIH_MGC Library."
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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90.03%
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/ case "male"
/ tissue_type="human embryonic stem cells differentiated to an early endodermal cell type"
/ cell type="human embryonic stem cells"
/ cell lipe="BG01"
/ lab host="bH10B-T1 phage-resistant E. coli"
/ clome lib="NIH MGC_258"
/ note="vector: pExpress-1; Site 1: Not!; Site 2: EccEV;
/ note="vector: pExpress-1; Site 1: Not!; Site 2: EccEV;
/ note="vector: pExpress-1; Site 1: Not!; Site 2: EccEV;
/ RNA obtained from human embryonic stem cells isolated from the inner cell mass of blaatocyst stage embryos and differentiated to an early endodermal cell type. Cell line id and NIH Registry designation is BG01. Positive for GATA4, MixLi, MaxI, HNR4alpha expression; negative for AFP expression. Passage number 40. CDNA primed using oligo-dry primer: 5'-pGACTAGTTCTAGATCGGAGGGGCCCCC(7:25-3' and cloned into the EcoRV/Not! sites of pExpress-1. This primary library is non-normalized (normalized brimary library is NIH MGC_259). It was constructed by Express Genomics (FredericE, MD). Sequence ends have been trimmed to exclude polya. Note: Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Note: this is a Mammalian Gene Collection library."
LeuProProValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeu 157
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Matches:
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/db_xref="taxon:9606"
/clone="IMAGE:7965451"
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DR156725
DR156725.1 G1:67868885
BST.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                          ValAlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIle
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1 (Dassel 1 to 826)

NHH-MGC Hetp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Dancel S. Gerhard, Ph.D.
Office of Cancer Genomics
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Homo sapiens
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/dev_stage="Adult"
/clone_lib="Mouse Neurosphere Normalized cDNA_library"
/clone_lib="Mouse Neurosphere Normalized cDNA_library"
/note="Corgan: Adult brain; Vector: pCMVSport6.0; A cDNA_library was constructed in pCMVsport6.0 from RNA isolated from neurospheres of adult male and female mice. Custom normalized cDNA_library by Invitrogen/ResGen"
                                                                                                                                                                                                                                                                                                                                        SerSerCysPheCysTyrLysHisTyrCysLysSerIleSerSerArgGlyArgTyrAsn 190
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Conservative:
Mismatches:
Indels:
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MNS07540 Mouse Neurosphere Normalized CDNA library Mus musculus CX204646.

MNS07540 Mouse Neurosphere Normalized CDNA library Mus musculus CX204646. GI:56859818

STT.

Mus musculus (house mouse)

Schurognathi, Muroidea, Murinae, Mus.

Expressed sequence tags of cDNA clones from murine neurospheres

Unpublished (1206)

Contact: Williams, C.

Molecular Biotechnology

Institution of Biotechnology

AlbaNow University Center, KTH-Royal Institute of Technology, 106

1 the Scholm, Sweden

Tel: 446855378431

Email: cecilia.williams@biotech.kth.se

Seq primer: MJSRM:

Locatia.millians.
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                                                                                                                                                                                                                                                                                                                                        GCTGCCTGTGGTCTGTGCCACCTGCACACAAATTTATGGCACCCCAAGGAAAGCCCGCA
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   GCATTTATTCCAGTTGGAGAATCACTAAAAGACCTTATTGACCAGTCACAAAGTTCTGGT
                                                 AGTGGGTCTGGACTACTTTATTGGTTCAGCGAACTATTGCCAAACAGATTCAGATGGTC
                                                                                                            GTGGCGGTGAAAGTATTCTTTACCACTGAAGAAGCCAGCTGGTTTCGAGAAACAGAAATC
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                                 SerGlySerGlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetVal
                                                                                                                                                       ValAlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIle
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/cell_type="Barly passage neurosphere"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
|mol_type="mRRA"
|fstrain=[C57BL/6"
|db_xref="taxon:10090"
|sex="MALE"
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CF744610 783 bp mRNA linear EST 10-OCT-2003 UI-M-GV0-clt-d-20-0U.rl NIH BMAP_GV0 Mus musculus cDNA clone IMAGE:30617467 5', mRNA sequence.
                                                                                                                                              CGTTACAACCGTGATTTGGAACAGGATGAAGCATTTATTCCAGTAGGAGAATCATTGAAA. 360
                                                                                                                                                                                                                                                                                                     AspLeulleAspGlnSerGlnSerSerGlySerGlySerGlyLeuProLeuLeuValGln 227
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Email: Ggapbe-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
                                                                                                                                                                                                                           ArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIleProValGlyGluSerLeuLys 207
                                                                                                                                                                                                                                                                                                                                         361 GACCTGATTGACCAGTCCCAAAGCTCTGGAGTGGATCTGGATTGCCTTTATTGGTTCAG 420
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Mus musculus
Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Glires, Rodentia,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
I (bases 1 to 783)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
 AsnLeuCysAsnGlnTyrLeuGlnProThrLeuProProValValIleGlyProPhePhe
                       121 AATTTGTGCAACCAGTATTTGCAGCCTACACTGCCCCCTGTTGTTATAGGTCCGTTCTTT
                                                                        AspGlySerValArgTrpLeuAlaValLeuIleSerMetAlaValCysIleValAlaMet
                                                                                              661 ATTACTGATTACCATGAAAATGGATCTCTCTATGACTTCCTGAAATGTGCCACACTAGAC
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                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
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This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                       1 (bases 1 to 779)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                           musculus (house mouse)
                                                                                                       CK638737.1 GI:41364603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.53e-142
1353.00
99.22%
98.44%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: pYX-5
                                                                                                                                                              Mus musculus
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Best Local Similarity:
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Pred. No.:
                                                                                                                                             Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                             DEFINITION
                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                  ACCESSION
                                                                                                   VERSION
KEYWORDS
SOURCE
       CK638737
LOCUS
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/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU124052
AU124052 NTZRM2 Homo sapiens cDNa clone NT2RM2001576 5', mRNA
                                                                                601
                                                                                                                                      306
                                                                                                                                                                                                 661
                                                                                                                                                                                                                                                       rLeulleThrAspTyrHisGluAsnGlySerLeuTyrAspDheLeuLysCysAlaThrLe 326
                                                                                                                                                                                                                                                                                                               721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Salto,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
Unpublished (2000)
Unpublished (2000)
Con oct 23, 2000 this sequence version replaced gi:55779243.
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.
1 (bases 1 to 807)
Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                      326 uAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHis 344
                                                                                                                                                                                                                                                                                                                                                                                                         807
261
3
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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1342.00
98.14%
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Homo sapiens
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KEYWORDS
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                                                                                                                                                                                     /tissue type="whole brain"
/dev_stage="1.5, and 15 days newborn"
/dote="Dysue in the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of the intervent of sequence located between the Not I site and the polya is GCAACTGAAT. This library was created for the University lows Brain Anatomy Project (BWAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ePheAspGlySerValArgTrpLeuAlaValLeuIleSerWetAlaValCysIleValAl 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 GluGluAspAspGln-GlyGluThrThrLeuThrSerGlyCysMetLysTyrGluGlySe 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 rAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArgThr1leGluCysCysAr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 TGATTTTCAATGCAAGGATTCACCGAAAGCCCAGCTACGCAGGACAATAGAATGTTGTCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 GGCTCGTTACAACCGTGATTTGGAACAGGATGAAGCATTTATTCCAGTAGGAGAATCATT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yGluValTrpMetGlyLysTrpArgGlyGluLysValAlaValLysValPhePheThrTh 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 GACCAATTFGTGCAACCAGTATTTGCAGCCTACACTGCCCCCTGTTGTTATAGGTCCGTT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 TATGATCATCTTCTCCAGCTGCTTTTGCTATAAGCATTATTGTAAGAGTATCTCAAGCAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGAAGATGAAGGGAGAACCACATTAACTTCTGGGTGTATGAAGTATGAAGGCTC
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253
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Matches:
Conservative:
Mismatches:
Indels:
                          1. .783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-600-645-2 (1-532) x CF744610 (1-783)
Location/Qualifiers
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1342.00
98.46%
97.68%
47.29%
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                                source
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9
  FEATURES
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/tissue type="whole eye"
/dev stage="whole eye"
/dev stage="whole eye"
/dev stage="whole (Ti phage resistant)"
/clone lib="NIH BMAP HZO"
/clone lib="NIH BMAP HZO"
/clone lib="NIH BMAP HZO"
/clone lib="NIH BMAP HZO"
/note="Organ: Bye; Vector: pXX-Asc; Site_l: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel:First strand cDNA synthesis was primed with oligc-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
       "Sciurognath; Muroidea; Muridae; Gilfes; Kodentia; Sciurognath; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 763)

2 In the MgC http://mgc.nci.nih.gov/.

1 (bases 1 to 763)

2 In the MgC http://mgc.nci.nih.gov/.

2 In the MgC http://mgc.nci.nih.gov/.

2 In the Robert Straubberg, Ph.D.

2 Email: cgapbs-r@mail.nih.gov

7 Tissue Procurement: Dr. James Lin University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefil.html

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 AlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGlu 313
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .763
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/strain="C57BL/6"
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DB:
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AUTHORS
TITLE
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COMMENT
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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KEYWORDS
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GlyserCysCysIleAlaAspLeuGlyLeuAlaValLysPheAsnSerAspThrAsnGlu 393 	ValaspileProLeuasnThrargValGlyThrargArgTyrMetAlaProGluValLeu 413 	AspGluSerLeuSerLysAsnHisPheGlnProTyrIleMetAlaAspIleTyrSerPhe 433 	GlyLeuileileTrpGluMetAlaArgArgCysileThrGlyGlyIleValGluGluTyr 453 	GInLeuproTyrTyrasnMetValbroSerAspProSerTyrGluAspMetArgGluVal 473 	ValCysValLysArgLeuArgProlleValSerAsnArgTrpAsnSerAspGluCysLeu 493 	ArgAlaValLeuLysLeuMetSerGluCysTrpAlaHisAsnProAlaSerArgLeuThr 513 	AlaLeuArglleLysLysThrLeuAlaLysMetValGlu 526
GlyserC GGAAGTT	ValAspi GTTGACA	AspGluS GATGAAA	GlyLeuI GGTTTGA	GlnLeuP CAATTAC		-	
374	394	414	434	454 543	474	494	514
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Search completed: December 9, 2005, 22:23:00 Job time : 4028 secs

307, Appli 1, Appli 5, Appli 5, Appli 37, Appl 116, App

5, Appli 18, Appl

OM protein

Run on:

Sequence:

Searched:

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Sequence 116, App. Sequence 5, Appli Sequence 85, Appli Sequence 137, Appl
                                                                                                                                                                                    Sequence 49, Appl
Sequence 2286, A
Sequence 2286, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 117, Appl
Sequence 86, Appl
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STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
US-09-903-068-13

US-10-739-413-13

US-10-641-319-3

US-10-745-237-307

US-10-153-217-1

US-09-903-068-5

US-09-903-068-5

US-09-903-068-5

US-10-66-152A-37

US-10-739-413-5

US-10-450-135-858-49

US-10-450-763-22861

US-10-450-763-22868

US-10-128-558-49

US-10-129-051-3

US-10-169-051-3

US-10-169-051-3

US-10-189-051-3

US-10-189-051-3

US-10-295-027-880

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Sequence 1, Application US/09874628
Sequence 1, Application US/09874628
Sequence 1, Application US/09874628
Sequence 1, Application US/09874628
GENERAL INCORMATION:
CELESTE, Anthony J.
THIES, R. Scott
YAMAJI, No. US20020137133A10TU
TITLE OF INVENTION: RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/874,628
FILING DATE: 05-Jun-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
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FILING DATE: 17-SEP-1993
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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  Sequence 1, Appli
Sequence 11, Appli
Sequence 121, App
Sequence 90, Appl
Sequence 119, App
Sequence 119, App
Sequence 88, Appl
Sequence 89, Appl
                                                                                           (without alignments)
5464.980 Million cell updates/sec
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Sequence 88, A
Sequence 89, A
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                                                                              December 9, 2005, 21:16:39; Search time 805 Seconds
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1: /cgn2 6/ptodata1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata1/pubpna/USO9_PUBCOMB.seq:*
3: /cgn2_6/ptodata1/pubpna/USO9B_PUBCOMB.seq:*
4: /cgn2_6/ptodata1/pubpna/USO9B_PUBCOMB.seq:*
5: /cgn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq:*
6: /cgn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq:*
8: /cgn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq:*
9: /cgn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq:*
9: /cgn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq:*
10: /cgn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                       - nucleic search, using frame_plus_p2n model
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US-10-600-645-1
US-10-463-190-121
US-10-868-497-90
US-10-463-190-119
US-10-463-190-120
US-10-868-497-88
US-10-868-497-88
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                                                                                                                                                                                                                                            9793542 segs, 4134689005 residues
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                                                                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Publication No. US20040142417A1
GENERAL INFORMATION:
APPLICANT: WOZNEY, John
CELESTE, Anthony of THIES, R. Scott
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US-10-600-645-1
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 5851
TELEPAK: 617 876 5851
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANDEDRESS: 81ngle
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                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
                                                                                                                  LOCATION: 61.,1656
SEQUENCE DESCRIPTION: SEQ
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100.00%
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                                                                                             CLONE: CFK1-23a
                                                                                                           NAME/KEY:
                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                     INFORMATION
                                                                                                                                US-09-874-628-1
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AlaargargCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
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                                                                                                                               ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeu1leSerMet
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               MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg
                                                                       ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro
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      TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
STREET: 87 CambridgePark Drive
CITY: Cambridge
CITY: Cambridge
STREET: 87 CambridgePark Drive
CITY: Cambridge
STREET: 87 Cambridge
STREET: 87 Cambridge
STREET: 87 Cambridge
STREET: 87 Cambridge
STREET: 87 Cambridge
COUNTRY: USA
ZIP: 02.40
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/600,645
FILING DATE: 23-Jun-2003
CLASSIFICATION: 530
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION UNUBER: US/08/123,934A
FILING DATE: 17-SEP-1993
ATTORNEY AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELEFORMINICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID
US-10-600-645-1
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LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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YAMAJI, Noboru
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Sequence 90, Application US/10868497
Fublication No. US20050106683A1
GENERAL INFORMATION:
APPLICANT: Winkler, David G.
APPLICANT: Shi, Jiye
APPLICANT: Latham, John
TITLE OF INVENTION: METHODS FOR INCREASING BON
TITLE OF INVENTION: METHODS FOR INCREASING BON
TITLE OF INVENTION: METHODS FOR INCREASING BON
CURRENT APPLICATION NUMBER: US/10/868,497
CURRENT APPLICATION NUMBER: US/10/866,497
CURRENT APPLICATION NUMBER: US/10/866,497
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 90
LENGTH::3003
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; ORGANISM: Rattus norvegicus
US-10-868-497-90
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Best Local Similarity:
Query Match:
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Pred. No.:
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             GCTGTCTGTATTGTCGCCATGATCGTCTTCTCCAGCTGCTTCTTGTTACAAACATTACTGT
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APPLICANT: Brunkow, Mary E.
APPLICANT: Galas, David J.
APPLICANT: Galas, David J.
APPLICANT: Mulligan, John T.
APPLICANT: Willigan, John T.
APPLICANT: Winkler, David G.
TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR TITLE OF INVENTION: INFORMATION COMPOSITIONS AND MEHTODS FOR TITLE OF INVENTION: LINCREADING BONE MINERALIZATION FILE REPERENCE: 2003-06-16
CURRENT FILING DATE: 2003-06-16
NUMBER OF SEQ ID NOS: 143
SEQ ID NOS: 143
SEQ ID NO:19
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Matches:
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Sequence 119, Application US/10463190
Publication No. US20040009535A1
GENERAL INFORMATION:
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                              S-10-463-190-120
Sequence 120, Application US/10463190
Publication No. US20040009535A1
GENERAL INFORMATION:
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                 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe
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Publication No. US20050106683A1
GENERAL INFORMATION:
APPLICANT: Winkler, David G.
APPLICANT: Shi, Jiye
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    US-10-868-497-88

Sequence 88, Application US/10868497

Sequence 88, Application US/10868497

Publication No. US20050106683A1

GENERAL INFORMATION:

APPLICANT: Winkler, David G.

APPLICANT: Shi, Jiye

APPLICANT: Latham, JOHN

TITLE OF INVENTION: MITHODIES SPECIFIC FOR SCLEROSTIN AND

TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION

FILE REPERENCE: 60117-128

CURRENT FILING DATE: 2004-06-15

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 88

LENGTH: 3167
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; ORGANISM: Rattus sp.
US-10-868-497-88
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Best Local Similarity:
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APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
Having Serine Threonine Kinase Domains And Their Use
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  LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGlulleTyrGlnThr
                                             AAAGTATTTTTTACCACTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACG
                                                                                                SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe
                                                                                                          TCCTGGACTCAGCTGTATTTGATTACTGATTACCATGAGAATGGGTCTCTCTATGACTTC
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Patent No. US20020123139A1
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei, Di
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
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US-09-903-068-13
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Matches:
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Mismatches:
Indels:
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APPLICANT: Latham, John
TITLE OF INVENTION: AWTHBODIES SPECIFIC FOR SCL
TITLE OF INVENTION: METHODS FOR INCREASING BON
FILE REFERENCE: 60117-128
CURRENT APPLICATION NUMBER: US/10/868,497
CURRENT FILING DATE: 2004-06-15
NUMBER OF SEQ ID NOS: 112
SOFTWARE FEASTSEQ for Windows Version 4.0
SEQ ID NO 89
LENGTH: 3167
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Best Local Similarity:
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TYPE: DNA
ORGANISM: Rattus
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys
                                      kb storage
                                                                                                                                                                            FILING DATE: 17-No. US20020123139A1ember-1993
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. US20020123139A1ember-1992
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9304680.3
APPLICATION NUMBER: 931047.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2070
526
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Matches:
Conservative:
Mismatches:
Indels:
                                     360
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         ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
PILING DATE: 11-0ul-2001
PRIOR APPLICATION DATA:
                                                                                                                                     APPLICATION NUMBER: 09/679,187
FILING DATE: «Unknown»
APPLICATION NUMBER: PCT/GB93/02367
                                                                                                                                                                                                                                                                                                                                                                                   NAME: KOhlei, Vineet
REGISTRATION NUMBER: 37,003
TELERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                FILING DATE: 28-May-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 217..1812
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 15-October-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAK: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
2823.00
99.81%
98.87%
99.47%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-600-645-2 (1-532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-903-068-13
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Db 337 CAGAAGACCAGAAAATGGAGTGACTTTAGCACCAGAGGATACCTTGCCTTTCTTAAAG 39 Qy 61 CysTyrCysSerGlyHisCysProAspAspAla1leAsnAsnThrCyslleThrAsnGly 80 	Qy 81 HisCysPhealaileileGluGluaspaspGlnGlyGluThrThrLeuThrSerGlyCys 100 Db 457 CATTGCTTTGCCATTATAGAAGATGATCAGGGAGAAACCACATTAACTTCTGGGTGT 516	Oy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 12	Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 14 bb 577 ACAATAGAATGTTGCGAACCAATTTGTGCAACCAGTATTGCAGCCTACACTGCCCCT 63	Qy 141 ValVallleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeulleSerMet 16	Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 18 Db 697 GCTGTCTGTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTTGCTATAAGCATTATTGT 75	Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnaspGluAlaPheIle 200 Db 757 AAGAGTATCTCAAGCAGGGTCGTTACAACCGTGATTTGGAACAGGATGAAGCATTATT 816	1 6		Oy 241 GlybysGlyArgTyrGlyGlyGlTrpMetGlybysTrpArgGlyGlubysValAlaVal 260	Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280	Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLySGlyThrGly 300 Db 1057 GTGTTAATGCGTCATGAAAATATACTTGGTTTTATAGCTGCAGACATTAAAGGCACTGGT 1114	Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320	Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340 Db 1177 CTGAAATGTGCCACACTAGACACCAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTTGT 1230	Qy 341 GlyLeuCy8HisLeuHisThrGluleTyrGlyThrGlnGlyLy8ProAlaIleAlaHis 360	361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsc 38 	Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400	Oy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
	9	9	v					CORRESPONDING								0	
Db 1417 AGGGGGCACCAAGCGGTACATGGCTCCAGAAGTGCTGGATGAAAGCCTGAATAAAAC 1470 Oy 421 HisPheGlnProTyrIleMetalaAspIleTyrSerPheGlyLeullelleTrpGluMet 440	Oy . 441 AlaargargCysIleThrGlyGlYJJEValGluGluTyrGlnLeuProTyrTyrAsnMet 460	Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480	171	520	Oy 521 LeualaLysMetValGluSerGlnAspValLysIle 532 		; Publication No. US20050048607A1 ; GENERAL INFORMATION: ; APPLICANT: MIYACONO, Kohei ; APPLICANT: IMAMURA, Takeshe	APPLICANT: DEN DIJKE, Peter TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE FILE REFERENCE: LUD 5539.1 CIP			S S E		0 2823.00 99.81%	98.87% Mismatches: 99.47% Indels: 9	-2 (1-532) x US-10-739-413-13 (1-2070) MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis	21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspV	rGGAC eurys

Pred. No.:	191	181 LysSerileSerSerArgGlyArgTyrAsnargAspLeuGluGlnAspGluAlaPhelle
0y 421 HisPheGlnProTyrileMetAlaAspileTyrSerPheGlyLeuIleIleTrpGluMet 440 14// CATTTCCACCCTACATCATGGCTGACATCTATAGCTTTGGTTTTGGGAATG 1536 441 AlaArgArgCyslleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460 1537 GCTCGTCGTTGTTTACAGGAGAATCTGGGAATTACCATTACAACATG 1596 461 ValProSerAspProSerTyrGluAspMetArgGlvAlValCysValLysArgLeuArg 480 1597 GTCCCAGTGACCCATCTATGAGGACATCGTGGAATTACCATTACAACATG 1596 Oy 481 ProlleValSerAshArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500 1657 CCAATCGTCTTATAGGGACAGCGAATGTCTGTGGAAACGCTTGCGG 1656 Oy 691 ProlleValSerAshArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500 1657 CCAATCGTCTAACGGCACAGGCGATGAATGTCTTCGAGCAGTTTTGAAGCTAATG 1716 Oy 692 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520 1717 TCAGAATGTTGGGCCCATAATCCAGCCTCCAGACTTTGAGAATCAAGACA 1776 Oy 521 LeuAlatysMetValGluSerGluAspValLysile 532	Db 1777 CTTGCAAAATGGTTGAATCCCAGGATGTAAAGAT 1812 RESULT 11 'Sequence 11, Application US/09742153 'Sequence 11, Application US/09742153 'Publication No. US20030096296A1 'GENERAL INFORMATION: 'TILE OF INVENTION: The Use of a BMP Protein Receptor Complex for Screening Bone Metabolism Actives and Cells CO-Transfected With a Type II BMP Receptor NUMBER OF SEQUENCES: 39 CORPESSER: The Procter & Gamble Company STREET: 11810 East Miami River Road CITY: Ross COUNTRY: USA COUNTRY: USA STREET: 45061 COMPITED PRADRAILE FORM.	COMPUTER: IEM PC compatible COMPUTER: IEM PC compatible COMPUTER: IEM PC compatible COMPUTER: IEM PC compatible COMPUTER: IEM PC compatible CURRENT APPLICATION DATA: APPLICATION NUMBER: US/0/142,153 FILING DATE: 20-Dec.2000 CLASSIFICATION: AUMENNON- PRIOR APPLICATION NUMBER: 08/462,467 FILING DATE: 05-JUN-1995 ATTORNEY/AGENT INNORMATION: NAME: Hersko, Bart S. REGISTRATION NUMBER: 32,572 REFERENCE/DOCKET NUMBER: 32,572 REFERENCE/DOCKET NUMBER: 5474R TELECOMONICATION INNORMATION: TELECOMONICATION INNORMATION: TELECOMONICATION INNORMATION: TELECOMONICATION INNORMATION: TELECOMONICATION INNORMATION: TELECOMONICATION INNORMATION: TELECOMONICATION INNORMATION: TELECOMONICATION INNORMATION: TELECOMONICATION INNORMATION: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic) SEQUENCE TYPE: DAMA (genomic)

Oy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPhelleIleSerHii 	21 ValGinGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspV 	Qy 41 GlnLysEysProGludsnGlyValThrLeuAlaProGludspThrLeuProPheLeuLys	Oy 61 CysTyrCysSerGlyHisCysProAspAspAlalleAsnAsnThrCysIleThrAsnGl;	Qy 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCy	Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg	Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro Db 651 ACAATAGAATGTTGTCGGACCAATTTGTGCAACCAGTATTTGCAGCCTACACTGCCCCT	Qy 141 ValValileGlyProPhePheAspGlySerValArgTrpLeuAlaValLeulleSerMet	Oy 161 AlaValCysIleValAlaMetIleValPheSerSerCy8PheCy8TyrLy8HisTyrCy8	Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIl.	Qy 201 ProValGlyGluSerLeuLy9AspLeuIleAspGlnSerGlnSerSerGlySerGlySer	Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVa 	Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal	Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	Qy 281 ValLeumetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLySGlyThrGly	Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	. 321	Oy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis
321 LeulysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340 	lahis 3 CTCAT 1	361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380 	381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400 	401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420 	421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeulleIleTrpGluMet 440 	441 AlaargargCyslleThrGlyGlylleValGluGluTyrGlnLeuProTyrTyrasnMet 460 	461 ValProSerAapProSerTyrGluAspMetArgGluValValValCysValLysArgLeuArg 480 	481 ProlleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500 	501 SerGlucysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArglleLysLysThr 520 	521 LeualaLysMetValGluSerGlnAspValLysIle 532 	RESULT 12 US-10-641-319-3 ; Sequence 3, Application US/10641319		TITLE OF INVENTION: Hematopoietic Stem Cell Niche Cells FILE REFERENCE: 64928 CURRENT APPLICATION NUMBER: US/10/641,319 CURRENT FILING DATE: 2003-08-14	NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin version 3.2 SEQ ID NO 3 LENGTH: 2056	TYPE: DNA ORGANISM: Mus musculus -10-641-319-3	Length: Matches: Conservati	93.59% Mismatches: 98.59% Indels: 7 Gaps:

Score Stallativ 98.504	Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
1371	

Query Match: 97.57% Indels: 0 DB: 5 Gaps: 0	US-10-600-645-2 (1-532) x US-10-153-217-1 (1-2623) Oy 1 MetfhrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPhelleIleSerHis 20				181 TGCTATTGCTCAGGGCACTGTCCAGATGCTATTAATAACACATGCATAACTAATGGA81 HiscysPheAlaileileGluGluAspAsgGlnGlyGluThrThrLeuthrSerGlyCys	— ⊢ m		361 ACAATAGAATGTTGTGGACCAATTTATGTAACCAGTATTTGCAACCCACACTGCCCCT 141 ValvalileGlyProPhePheAspGlySerValArgTrpLeualaValLeulleSerMec			1	Qy 201 ProValGlyGluSerLeuLy8AspLeuIleAspGlnSerGlnSerGlySer 220	Qy 221 GlyLeuProLeuLeuValGlnArgThrileAlaLysGlnNetValArgGlnVal 240	Oy 241 GlyLysGlyArgTyrGlyValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260	Qy 261 LysValPhePheThrThrGludluAlaSerTrpPheArgGluThrGlulleTyrGlnThr 280	Oy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIlealaAlaAspIleLysGlyThrGly 300	Oy 301 SerTrpThrGlnLeuTyrLeuIleThraspTyrHisGluAsnGlySerLeuTyrAspPhe 320	Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340 	
Db 961 CTGAAATGTGCTACACTGGACACCCAGGCTCTTAAATTGGCTTATTCAGCTGCTTGT 1020	Oy 341 GlyLeuCysHisLeuHisThrGlulleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360 	Qy 361 ArgAspLeuLysSerLysBasnIleLeuIleLysBasnGlySerCysCysIlealaasp 380	Qy 381 LeuGlyLeuAlaValLySPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400 Db 1141 CTGGGCCTTGCTTAAATTCAACAGTGACACAAATGAAGTTGATGTGCCCTTGAATACC 1200	Oy 401 ArgValGlyThrArgArgTyrMetAlaBroGluValLeuAspGluSerLeuSerLysAsn 420 		Qy 441 AlaArgArgCys1leThrGlyGly1leValGluGluTyrGlnLeuProTyrTyrAsnMet 460 Db 1321 GCTCGTTGTTGTATCACAGGAGGATCGTGGAAGAATACCAATTGCCATATTACAACATG 1380	Oy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480 Db 1381 GTACCGAGTGATCCGTCATACGAGATATCGTGTGTGTCTCTCTC	ProlleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet	Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArg11eLysLysThr 520 	Oy 521 LeualaLysMetValGluSerGlnAspValLysIle 532 	SULT 14	; Sequence 1, Application US/10153217 ; Publication No. US20030072758A1 ; GENERAL INFORMATION:	; TITLE OF INVENTION: BMARS INVOLVEMENT IN JUVENILE POLYPOSIS; FILE REFERENCE: IOWA:037US ; CURRENT APPLICATION NUMBER: US/10/153,217 ; CURRENT APPLICATION 1000-06-21	PRIOR PELLICATION NUMBER: 60/292,691 PRIOR FILING DATE: 2001-05-21 NUMBER OF SEQ 1D NOS: 2	SOFTWAKE: Patentin Ver. 2.1 SOFTWAKE: Patentin Ver. 2.1 LENGTH: 2623 TYPE: DNA	OKGANISM: Artificial Sequence FEATURE: NAME/KEY: CDS COCATION: (1) (1596)	; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Primer US-10-153-217-1	Alignment Scores: Pred. No.: Score. Score. Percent Similarity: Best Local Similarity: 97.18 Mismatches:	

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HisCysPheAla11e11eGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTATTGCTCAGGGCACTGTCCAGATGATGCTATTAATAACACATGCATAATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTGCTTTGCCATCATAGAAGAAGATGACCAGGGAGAAACCACATTAGCTTCAGGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAAATATGAAGGATCTGATTTTCAGTGCAAAGATTCTCCAAAAGCCCAGCTACGCCGG
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517
7
8
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                ATTORNEY/AGENT INPORMATION:
NAME: KOHIE, Vinee
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March.1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-Auguser-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO: 5:
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 310.,1905
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 310..1905
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    internal
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2769.00
98.50%
97.18%
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
DB:
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Percent Similarity:
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TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1081 CGAGACCTAAAGAGCAAAACATCCTCATCAAGAAAATGGGAGTTGCTGCATTGCTGAC 1140
                                                                                                                                                                     1141 CTGGCCTTGCTGTTAAATTCAACAGTGACACAAATGAAGTTGATGTGCCCTTGAATAC 1200
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GlyLeuCysHisLeuHisThrGlulleTyrGlyThrGlnGlyLysProAlalleAlaHis
                                                                       ArgAspLeuLysSerLysAsnileLeulleLysLysAsnGlySerCysCysIleAlaAsp
                       1021 GGTCTGTGCCCCCCGCACACAGAAATTTATGGCACCCAAGGAAAGCCCGCAATTGCTCAT
                                                                                                                                                                                                                                                                                            HisPheGlnProTyr1leMetAlaAsp1leTyrSerPheGlyLeu1le1leTrpGluMet
                                                                                                                                                                                                                                                                                                                                                                      AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProlleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet
                                                                                                                                               LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr
                                                                                                                                                                                                                        ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn
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FILING DATE: «Unknown»
APPLICATION NUMBER: PCT/GB93/02367
LLING DATE: 17-NO. US20020123139Alember-1993
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-NO. US20020123139Alember-1992
FILING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1561 CTTGCCAAGATGGTTGAATCCCAAGATGTAAAATC 1596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 360 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/903,068
FILING DATE: 11-Jul-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
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Patent No. US20020123139A1
GENERAL INFORMATION:
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US-09-903-068-5
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